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length: 2000000000
                                                                       Query
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B1819200 603034614
BM921213 AGENCOURT
B1871711 603395825
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 source
      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11517 row: c column: 18
High quality sequence stop: 772.
Location/Qualifiers
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BI766766
BI766766.1 GI:
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 834)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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603056866F1 NIH_MGC_122 Homo
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BI870393
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BM971606 UI-CF-EC1
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BASE COUNT
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Matches 818; Conserv
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/db_xref="taxon:9606"
/clone="IMAGE:5206217"
/clone_11b="NIH_MGC_122"
/lab_host="DH10B"
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ACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACCTGTACTGTCAGG
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BO707185 BQ707185.1 GI:21846084 EST.
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807; Conserv
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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High quality sequence stop: 550.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 948)
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National Institutes of Health, M
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/lab_ho
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cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2456 row: 1 column: 13
High quality sequence stop: 565.
Location/Qualifiers
                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 963)
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AGENCOURT_B303564 NIH_MGC_102
5', mRNA sequence.
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//clone_lib="NH_MGC_102"
//tissue_type="epidermoid carcinoma, cell line"
//lab_host="DH10B (phage-resistant)"
//note="Organ: salivary gland; vector: poTB7; Site_1: xhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/xhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
94 a 326 c 260 g 183 t
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/db_xref="taxon:9606"
/clone="IMAGE:6274716"
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                           TGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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plate: LLAM11437 row: l column: 03
High quality sequence stop: 759.
Location/Qualifiers
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603034614F1 NIH_MGC_115
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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                                                                                                                                                                                          /note-*Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5175698"
/clone_lib="NIH_MGC_115"
                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                      found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM12786 row: p column: 02
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/db_xref="taxon:9606"
/clone="ib-"NIH_MGC_115"
/clone_lib-"NIH_MGC_115"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-*Organ: pooled brain, lung, testis; vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12034 row: b column: 07
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 731)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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603395825F1 NIH_MGC_90
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/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

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/db_xref="taxon:9606"
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                                                                                                         Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), S
cDNA Library Preparation: Michael J. Brownstein (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11722 row: k column: 13
High quality sequence stop: 776.
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1 (bases 1 to 828)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5285892"
/clone=lib="NIH_MGC_96"
/tissue_type="Nypothalamus"
/lab_host="DH10B"
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RESULT 8 B1870393

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IMAGE:

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Pred. No. 7.8e-140;
0; Mismatches 30;
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                                                   CCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACCTGTACTGTCAGGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1 (bases 1 to 728)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5405459"
/clone_lib="NIH_MGC_90"
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/tab.host="DH10B (phage-resistant)"
/note="organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC_Library."
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Pred. No. 1.6e-137;
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MA 02138
                                                                                                                                                                                                                                                             Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA se
Washington University Genome Sequencing Center For i
obtaining a clone please contact: Juliana Brown
(brownefas.harvard.edu) This sequence now available
consortium, for clone orders contact: info@image.lln
High quality sequence stop: 412.
Location/Qualifiers
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Harvard University, Howard Hughes Medical
Dept of Molecular and Cellular Biology, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Douglas Melton, Klaus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hillier, L., Marra, M., Pa
Schmitt, A., Theising, B.,
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Lemishka, I., Scearce,
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1 (bases 1 to 609)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 617-495-8557
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note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not I Site_2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). made by oligo-dT priming. Size-selected by column
                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5672623"
                                                                                                   /tissue_type="Islets of Langerhans"
/dev_stage="Adult"
                                                                                /lab_host="DH10B"
                                                                                                                                             /sex="Both"
                                                                                                                                                                  /clone_lib="Melton Normalized
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Primates;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1027)
Cousin.P., Billotte.J., Chaubert.P. and Shaw.P.H. Physical map of 17p13 and the genes adjacent to p53 Genomics 63 (1), 60-68 (2000)
                                                                                           Homo sapiens
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                                                                                                                                                     AAAACAGATATTATTTATTATTATTATTGTGACAAAATGTTGATAAATGG 1373
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Institute of Pathology
Rue du Bugnon 25, Lausanne, VD 10
sub_clone=AB2R Asc-BamHI PSL1180
Class: BAC subclone.
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Contact:
                                                        BQ884231 940 bp mRNJ
AGENCOURT_8682031 Lupski_sciatic_nerve
IMAGE:6197488 5', mRNA sequence.
 Homo
            human.
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/clone_lib="Human"
/note="Vector: pMOS E
a 317 c 282 g
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/db_xref="taxon:9606"
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CAGCTCCGCCTCTG-CCAGGTGTCTGGGCCTGTTGGCCCTGCGGCCA-GGGTCCTCCCTGC
                                                GTGCTGGCCCTGCGCTGCAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGGCCC 720
                                                                                                                                                         GTGCTGGCCCTGCGCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGGCCC
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                                                                                                                                                                                                                                                                                      660;
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM13607 row: j column: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-*Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by Oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCTCCG-3' and 5'-GACTACTTCTAGATCCGACCGCCCCCT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6197488"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult,
/lab_host="DH10B"
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/dev_stage="adult, 70 yr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Lupski_sciatic_nerve"
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96.58;
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                   Genetics (www.resgen.com).
The following repetitive elements were sequence: 1-82, >NT_rich#Low_complexity
Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
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1 (bases 1 to 568)
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/tissue_type="Lung"
/tissue_type="Lung"
/dev_stage="Adult and Fetal"
/lab_host="DH108 (Life Technologies) (T1 phage resistant)"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; U1-CF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Res.
                                                                                                                                                                                                                                      /clone="UI-CF-EC1-ab1-p-06-0-UI"
/clone_lib="UI-CF-EC1"
                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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Contact: Robert Strausberg, |
Email: ggapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/lab_host="Dell'08 (phage-resistant)"
/note="organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
/note="organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed
Average insert size 1.533 kb. Library enriched for
full-length clones and constructed by Life Technologies
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BI824443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI824443
603038693F1 NIH_MGC_115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                            72
                                                                                                                                                                                                                                                                                                                                                     /note-*Organ: pooled brain, lung, testis; Vector: pCMV-SPORTG; Site_1: NotI; Site_2: ECORV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:5179510"
/clone_11b="NIH_MGC_115"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ∕organism="Homo sapiens"
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Pred. No. 1.7e-102;
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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Contact: Robert Strausberg, Ph.D.
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plate: LLAM9767 row: p column:
High quality sequence start: 17
High quality sequence stop: 724.
Location/Qualifiers
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National Institutes of Health, Mammalian
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:4206595"
/clone=lib="NCI_CGAP_CO24"
/clone=lib="NCI_CGAP_CO24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1:
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: pCMV-SPORT6; Site_1:
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: pCMV-SPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="FVB/N"
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86.9%;
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                                                                                                                                                                     Score 493.6; DB 1
Pred. No. 2.2e-97;
                                                                                                                                       Mismatches
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Search completed: March 31, 2003, 11:47:36 Job time: 2533.03 secs

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ALIGNMENTS

RESULT 1
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ID AAV1

AAV18600 standard; cDNA; 1373 BP

21-JUL-1998 (first entry)

AAV18600;

18-MAR-1997; 07-AUG-1996; 18-OCT-1996; TRELL; tumour necrosis factor related ligand; tnf; treatment; cancer; autoimmune disease; immune system; stimulation; suppression; graft rejection; ds.. (BIOJ) BIOGEN INC 07-AUG-1997; 12-FEB-1998 WO9805783-A1 Homo sapiens Homo sapiens tumour necrosis factor related ligand (TRELL) gene. 97US-0040820. 96US-0023541. 96US-0028515. 97WO-US13945 Location/Qualifiers
1..852 /note= /*tag= a "tumour necrosis factor related ligand"

Expression vector

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standard; cDNA;

08-MAY-2002 (first entry)

CDNA secreted protein #19

Human; secreted protein; gene; ss; nutritional supplement; haemophlli viral infection; bacterial infection; fungal infection; diabetes; ast autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulc diabetes; asthma; haemophilia; tumour;

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                                                                                                                                                                                                                                                                                                                           CC a variety of human tissue sources and which encode novel secreted CC proteins. The polynucleotides can be used as probes for the CC identification and isolation of full length cDNA and genomic DNA. The CC identification and isolation of full length cDNA and genomic DNA. The CC and proteins are useful in the treatment of various immune deficiencies CC and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple CC sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's CC disease), liver fibrosis, coagulation disorders (e.g. haemophilia), CC useful for tissue regeneration, for wound healing and in the treatment of Durns, inclisions and ulcers. The proteins are also useful for regulating CC haematopoiesis and for treating myeloid or lymphoid cell deficiencies. Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
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                                                                         TGCCTCGGCCTGCTGGCCGTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAG
                                                                                     TGCCTCGGCCTCCTGCTGGCCGTGGTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAG
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                                                                                                                         GGGGAGCCGGCCACCGCCCTGCTGGTCCCGCCTCGCGCCTGGGCCTGGCCCTGGCCCT
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Pred. No. 4.3e-277;
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Best Local Similarity
Matches 1337; Conserv
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Pred. No. 1.2e-272;
0; Mismatches 20;
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JNK/SAPK-dependent res
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                                                              GACCTGGCGCAGGAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGG
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The present sequence is that of cDNA clone DNA30879-1152

(APCC 209358) encoding human PRO207 (see AAY95338), which shows homology to several members of the tumour necrosis factor family, especially human lymphotoxin (23.4%). The cDNA was identified in a foetal kidney cDNA library following identification of an expressed sequence tag with homology to human Apo-2 ligand. A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell to PRO179, PRO207, PRO320, PRO219, PRO221, PRO224, PRO301, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866 (see CAX95337-49), their agonists or chimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder and central nervous system cancer, melanoma and leukaemia. Nucleic efficient and control of the condition of the condit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-MAR-1999;
21-APR-1999;
28-APR-1999;
14-MAY-1999;
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26-JUL-1999;
15-SEP-1999;
15-SEP-1999;
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PRO221, F
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                                                                                                                                                                                                                                                                                                                                         Claim 20;
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                                                                                                                                                                                                                                                                                                                                                                                          composition to inhibit neoplastic cell growth or in mammal comprises polypeptides PRO179, PRO207, 1, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; human; cancer;
                                      antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENENTECH INC.
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99US-0130232.
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99US-0134287.
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/*tag= b
178..804
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system cancer; melanoma;
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                                    polypeptides
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te cancer; lung cancer; bladder cancer;
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d WI;
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                                                                        GCCGGCTCCCCTCGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCACCCTCAGCCGCT
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Pred. No. 1.2e-271;
D; Mismatches 3;
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L RM; Roy MA,
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Smith
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                                             DM.
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Best Local Sim:
Matches 1322;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
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Pred. No. 1.2
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sue grafting; vascularisation; apoptosis; autoimmune; birth or
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                                                                                                                                                                                                                                                                                                                          CC The TNF-related endothelium proliferative agent (TREPA), or its cativators or agonists, are used to treat a deficit of TREPA, e.g. to promote wound healing or tissue grafting, by promoting vascularisation, calso to induce apoptosis for treating cancer and eliminating autoreactive T cells, as an adjunct to cancer chemotherapy or antiviral treatment. Crappa peptides can also be used to target cytotoxic agents or for caffinity isolation of the corresponding receptor, the nucleic acid for which can be used to transform tumour cells to render them more cresponsive to TREPA and to screen for TREPA mimics. Cresponsive to TREPA and to screen for TREPA mimics. Are used to treat TREPA-associated diseases, e.g. tumours and metastases (by inhibiting conditions involving abnormal stimulation of epithelial cells (e.g. atherosclerosis), for birth control (inhibiting ovulation and placental Cramation) or other angiogenic conditions (e.g. ulcers).
                                                                                                                                                                                                                                                                     Query Match
Best Local Sin
Matches 1230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting nucleic acid encoding TREPA - useful for diagnosis treatment of autoimmune disease, tumours and inflammation
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                                                                                                                                                             Similarity
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Best Local Similarity
Matches 1230; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molecules designated as TREPA (TNF related endothelium proliferative agent). Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis in human for promoting wound healing and for vascularising grafted tissue for successful grafting and to promote tissue grafts. The present sequence is a cDNA clone ID #690050 encoding human TREPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing angiogenesis in mammal at desired sites for promoting wound healing, by administering soluble fragment of extracellular domain of tumor necrosis factor related endothelium proliferative agent protein
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                                                                                                                                                                                                                                                                                                                                       domain; immunogen; antibody preparation;
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Query Match Best Local S Matches 834

Similarity

60.7%; ilarity 99.9%; Conservative

0;

Score 833.4; Pred. No. 4.8e 0; Mismatches

.8e-168; DB

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Indels Length

0; Gaps

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GTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGGAGCTGGTG

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61

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649 361 589 301 529 241 469 181 409 121 349

CTGGTGGATGGTGTGCTGGCCCTGCCCTGCGAGGAATTCTCAGCCACTGCGGCCAGT

708 420

TACCTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTG

648

588

300

360

AGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTAC

 ${ t AGCCCTCTGCGCTACTACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTAC}$

GCGCAGGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCC CGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACGGA CGGGCTCGAAGAGCGATCGCAGCCCATTATGAAGTTCATCCACGACCTGGACAGGACGGA GCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCCGGAAAACA

528 240 468 180 408 120

GCGCAGGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCC

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This invention describes isolated Tumor Necrosis Factor (TNF) family creceptor polypeptides: APO4, APO6, APO8 and APO9 or their active CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic comolety, APO4 polypeptides are also useful for identifying selective cc binding agents, useful in diagnosis/treatment of disease by binding of agents to the polypeptide/active fragment which is extracellular, or CC expressed on the cell surface. The binding is preferably performed in creatment of disease are also useful for screening creatment of disease are also identified using and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or cc treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vivo or in vitro. APO polypeptides are all useful as immunogens for preparing antibodies. APO4 is also cuseful for diagnosis/treatment of developmental or gestational cc abnormalities. APO8 was transfected to human breast carcinoma cell line were all useful apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Tumor Necrosis Factor family receptor polypeptides useful for diagnosis and treatment of prostate cancer \epsilon developmental or gestational abnormalities
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Sequence
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DB; AAW93590.
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other;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWEAK extracellular domain; tumour necrosis factor; TNF; angiogenesis; occular necvascularisation; diabetic retinopathy; necvascular glaucoma; retinoblascoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; ds; corneal graft necvascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint; preneoplastic condition; myocardial angiogenesis; wound granulation; scleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerosi; plaque necvascularisation; coronary atherosclerosis; peripheral atherosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAKR;
Wiley
                                                                             20-DEC-1999;
10-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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                                       (IMMV ) IMMUNEX CORP
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                                                                               2000US-0203347
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
52:.873
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                                                                                                    99US-0172878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pDC409-LZ-TWEAK fusion protein-encoding
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                                                                                                                                                                                                                                                             "Fusion protein comprising a growth hormone leader, a leucine zipper multimerisation domain, and human TWEAK extracellular domain"
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Best Local S
Matches 631
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                  CTCGGGCCCCAGCTCCGCCTCTGCCAGGTGTCTGGGCCTGTTGGCCCTGCGGCCAGGGTCC
                                                            GTGGATGGTGTGCTGGCCTGCGCTGCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCC
                                                                             GTGGATGGTGTGCTGGCCTGCGCTGCCTGCAGGAATTCTCAGCCACTGCGGCCAGTTCC
                                                                                                                                          CTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTG
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CC pDC409-LZ-TWEAK, which encodes a fusion protein computaing a growth CC hormone leader, a leucine zipper multimerisation domain, and the CC extracellular domain of human TWEAK. The fusion protein was used in the isolation of human TWEAK receptor (TWEAKR)-expressing clones CC from a COS cell human cDNA library. The TWEAKR protein is a CC member of the tumour necrosis factor (TNF) family and induces CC angiogenesis. TWEAKR may therefore be used to screen for and develop CC TWEAKR agonists and antagonists for the modulation of angiogenesis, to be CC used in the treatment and diagnosis of human disease. The disorders CC mediated by angiogenesis include ocular disorders characterised by ocular CC retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, CC rubeosis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, CC neovascularisation, and inflammatory diseases include malignant and CC metastatic conditions such as sarcomas and carcinomas, benign tumours and preneplastic conditions, myocardial angiogenesis, haemophilic joints, CC scleroderma, vascular adhesions, atherosclerotic plaque covascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac peripheral tissue, by administering antagonist or agonist of TWEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents a DNA from the expression vector pDC409-L2-TWEAK, which encodes a fusion protein comprisi
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P-PSDB; AAU03499.
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Similarity Conservative 45 99 5 8 0; Score 629.2; Pred. No. 1.4 Mismatches .4e-124; В 22; Indels Length 898 0 Gaps 0

187 A;

266 C;

267 G; 178 T;

0 other;

9;

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RESULT 10
AAV18599
ID AAV18599
ID AAV18599
ID AAV18599
ID AAV1
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The sequence is that encoding mouse tumour necrosis factor related carrier in pharmaceutical compositions to treat cancer, autoimmune cases or immune responses to tissue grafts, or to stimulate or suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for, can then be administered, optionally with interferon-gamma, to induce cell death or treat, suppress or alter immune responses (especially involving human adenocarcinoma cells) involving a signal pathway between TRELL and its receptor. The DNA sequence can be used in gene therapy for TRELL-related disorders in manmals (especially humans), e.g. tumours, autoimmune and inflammatory diseases or inherited genetic disorders, by introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL. It may also be of use in the preparation of prepare probes for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-1997;
07-AUG-1996;
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RESULT 11
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             This invention describes isolated Tumor Necrosis Factor (TNF) family receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer by determining levels of APO4 is useful for diagnosing prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic molety. APO4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding of agents to the polypeptide/active fragment which is extracellular, or expressed on the cell surface. The binding is preferably performed in vivo. APO4 polypeptides/ active fragments are also useful for screening for agenists and antagonists by binding and observing the changer in APO4 for the polypeptides of active fragments are also useful for screening for screening fragments are also useful for screening for the polypeptides of active fragments are also useful for screening for screening fragments are also useful for screening fragments are also useful for screening for screening fragments are also useful for screening for screening fragments are also useful for 
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                                                                                                                                                                                                                                                                                                                                                      New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4 developmental abnormality; gestational abnormalitity; prostate cancer; APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; diseacytoplasmic domain; immunogen; antibody preparation; breast carcinoma:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1312
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                                                                                                                                                                                                                                                                                                               Example
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P-PSDB; AAW93591.
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Effective
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WASHINGTON
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/*tag- a
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/product- "TNRL3"
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pharmacological agents useful
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diagnosis
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AAT22190 sta AAT22190; 27-AUG-1996

(first

entry)

standard;

CDNA

to mRNA;

gene

signature HUMGS03761.

Gene signature; messenger RNA; mRNA; human; cloning; mapping; non-biased l cell typing; abnormal cell function;

library;

diagnosis;

frequency;
detection;

relative abundance;

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RESULT 13
AAT22190
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Best Local S
Matches 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interac with a cytoplasmic domain of APO4 and detecting a change in level of APO activity. The method is performed in vivo or in vitro. APO polypeptides are all useful as immunogens for preparing antibodies. APO4 is also useful for diagnosis/treatment of developmental or gestational abnormalities. APO8 was transfected to human breast carcinoma cell line MCF-7, and induced apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                       CAGGATCCTGCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGC
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                                                                                                                           CGGCCAGGGTCCTCCCTGCGGATCCGCCACCCTCCCCTGGGCCCCATCTCAAGGCTGCCCCC
                                                                                                                                                                               GCGGCCAGTTCCCTCGGGCCCCAGCTCTGCCAGGTGTCTGGGCTGTTGGCCCTG
                                                                                                                                                                                                                                    CTGGACTTGCTGGTGGATGGTGTGCTGGCCCTGCGCTGCGGAGGAATTCTCAGCCACT
                                                                                                                                                                                                                                                                                       GGGCTCTACTACCTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAG
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                                                                                                               CGGCCAGGGTCTTCCCTTCGGATCCGCACCCTCCCCTGGGCTCATCTTAAGGCTGCCCCC
                                                                                                                                                                  GCAGCAAGCTCTCCTGGGCCCCCAGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGGCGCTG
                                                                                                                                                                                                                      CTGGACTTGCTGGTGAACGGTGTGCTGGCCTGCGCTGCCTGGAAGAATTCTCAGCCACA
                                                                                                                                                                                                                                                                           GGGCTCTACTACCTGTACTGTCAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAG
                                                                                                                                                                                                                                                                                                                                                                               CAGGATGGAGCACAAGCAGGTGTGGATGGGACAGTGGCTGGGAAGAGACCAAAATC
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87.3%;
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Pred. No. 3.4
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RESULT 13
ABK29540
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AC ABK29
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                                                                                                                                                                                                                                                                                                                   A single-stranded DNA (or its complementary strand or the corresp. C double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the G' '-end of mRNA by using poly(T) as the sole primer. Since the 3'-C untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                                                                                                                  1290
                                                                                                                                                                          1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                   ABK29540 standard; cDNA;
                                                                                                                                                                                                                                                       1111 GATCTCGACTCCCCCCTGGCCACAGACCCCCCAGGGCATTGTGTTCACTGTACTCTGTGGG 1170
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 1067; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OKUB/)
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                                                                                                               181
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                                                                                                                                                                                                                                                                            Local Similarity
nes 257; Conserv
                                                                                                                                                                                                                                  CAAGGATGGGTCCAGAAGACCCCACTTCAGGCACTAAGAGGGGCTGGACCTG-GCGGCAG 1229
                                                                                TTGTGACAAAATGTTGATAAATGG
                                                                                                                        CAAGCTCCTCCCTTGAGAATTCCCCTGTGGATTTTTAAAAACAGATATTATTATTATTATTA 1349
                                                                                                                                                               GAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCAAATGTGAGGGGCGAGAAACAAGA 1289
                                                                                                             CAAGCTCCTCCCTTGAGAATTCCCTGTGGATTTTTAAAAACAGATATTATTTTTNTNATTA 240
                                                                                                                                                     GAAGCCAAAGAGACTGGGCCTAGGCCAGGAGTTCCCCAAATNTGAGGGGCGAGAAACAAGA
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OKUBO K.
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                   BP;
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                                                                                                                                                                                                                                                                                                                  80 A; 62 C;
                                                                                                                                                                                                                                                                                    17.9%;
97.3%;
                      195
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                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                              Score 245.4;
                                                                                                                                                                                                                                                                                                                  69 G; 66 T; 5 other;
                                                                                         1373
                                                                       264
                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                             Length
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CC polypeptide (III) comprising a portion of a colon tumour protein. A new color tumour protein of a colon tumour protein for determining the presence of a cancer in a patient. (II) or antigen cC determining the presence of a cancer in a patient. (II) or antigen cC presenting cells expressing (I) are useful for stimulating and/or cC expanding T cells expressing (I) are useful for stimulating and/or cC expanding T cells specific for a tumour protein, by contacting T cells (I), (II), (II), (II), (II), (II), or antigen presenting cells that express (II) are useful for treating CC colon cancer in a patient by incubating CD4+ and/or CD8+ T cells isolated CC from a patient with (I), (II), or antigen presenting cells that express (II), so that T cells proliferate, and administering to the patient an CC effective amount of the proliferated T cells, thus inhibiting the CC development of a cancer in the patient. A new composition is useful for CC vaccines and pharmaceutical compositions for prevention and treatment of CC colon cancer and for the diagnosis and monitoring of the cancers. (I), (II) or an antibody against (II) is useful for detection, diagnosis and/or therapy of human colon cancer. (I) is useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of ribozyme colon cancers in thibiting expression of (II) in tumour cells. ABK29475—cc ABK29851 represent human colon adenocarcinoma-specific cDNA sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                            1250
                                                                                                                                                                                                                                                         1190
                                                                                                                                                                                                                                                                                                                                                       1130 CCACAGACCCCCAGGGCATTGTGTTCACTGTGACTCTGTGGGCAAGGATGGGTCCAGAAGA 1189
1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide (I) encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of colon tumour protein, colon cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide encoding a polypeptide comprising of colon tumour protein, for detection, diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-098052/13
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22-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meagher MJ, King GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
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                                                            121
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                                                                                                                                                                                                                                                                                                                         1 CCACAGACCCCCAGGTCATTGTGTTCACTGTACTCTGTGGGCAAGGATGGGTCCAGAAGA 60
TCCCTGTGGATTTT
                                                                                                                         TAGGCCAGGAGTTCCCAAATGTGAGGGGGGGGAGAAACAAGACAAGCTCCTCCCTTGAGAAT 1309
                                                                                                                                                                                                                          CCCCACTTCAGGCACTAAGAGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCC 1249
                                                            TAGGCCAGGAGTTCCCAAATGTGAGGGGGGGGAGAACAAGACAAGCTCCTCCCTTGAGAAT
                                                                                                                                                                                         CCCCACTTCAGGCACTAAGAGGGGGCTGGACCTGGCGGCAGGAAGCCAAAGAGACTGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 49 A; 51 C;
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2000US-252614P
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 193.4; DB 24; Pred. No. 5.7e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 G; 37 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secrist
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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TCCCTGTGGATTTTT

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RESULT 14
AAX53491,
                                                   Query Match
     Matches
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                                                                                                                                                                                                                            inflammation, including lung diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis, acute asthma, allergies, asthma, im respiration, respiratory distress syndrome, pain, cystic fibrosis, pulmonary hypertension, pulmonary vasoconstriction, emphysema, chron obstructive pulmonary disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer, lymphomas, carcinomas e.g. colon cancer, breast cancer, lung cancer,
                                                                                                                                     lymphomas, carcinomas e.g. colon cancer, preuse cancer, melanoma, pancreatic cancer, hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as well as all types of cancers which may metasta or have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs, including breast and prostate cancer have metastasized to the lungs.
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17-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pulmonary hypertension; pulmonary vasoconstriction; emphysema; chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma; colon cancer; breast cancer; lung cancer; pancreatic cancer; colon cancer; breast cancer; lung cancer; pancreatic cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     impaired respiration; inflammation; lung disease; pulmonary vasoconstriction; inflammation; allergic rhinitis; pulmonary vasoconstriction; inflammation; allergic rhinitis; acute asthma; allergy; asthma; impeded respiration; respiratory distress syndrome; pain; cystic fibrosis; respiratory distress syndrome; pain; cystic fibrosis;
                                                                                                          Sequence 114955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
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                             Local Similarity
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97US-0059160
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                                                                                                          BP;
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                                                                                                       6071 A;
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                           .5.1%;
32.7%;
  58;
                                                                                                       29417 C;
                           Score 70.4;
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Mismatches
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                                                                                                       36712 G;
                             .6e-05
                                                   DB 20;
  316;
                                                                                                    21328 T; 21427 other;
  Indels
                                                 Length 114955;
                                                                                                                                                                                 which may metastasize
                                                                                                                                                                                                                                                                                     emphysema, chronic
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28-JAN-1998;
24-FEB-1998;
31-MAR-1998;
03-APR-1998;
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(HYSE-)
   Crkvenjakov
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                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                       genetic analysis;
                                                                                                                                                                                                                                                     detection;
                                                                                                                                                                                                                                                                                       Human
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                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                    gene; gene expression product; diagnosis; therapy; probe;
ion; mapping; tissue typing; profiling; forensic; cancer;
                          CHIRON
HYSEQ 1
R,
                                                                                                                                                                                                                                                                                     expression product
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                                                             98US-0080666.
98US-0072910.
98US-0075954.
98US-0080114.
98US-0080515.
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     Dickson
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     Drmanac
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CC comprising the sequences given in AAZI2532 to AAZI7779. Also described is camerindo of detecting differentially expressed genes correlated with the CC cancerous state of a mammalian cell, comprising detecting at least one CC differentially expressed gene product in a test sample from a cell cosuspected of being cancerous, where the gene product is encoded by one CC of the 5248 polynucleotide sequences given in AAZI2532 to AAZI7779. The CC polynucleotides can be used as a source of primers and probes, which can be used for a variety of purpose, e.g. detection of expression levels, cm apphing, tissue typing or profiling, forensics, genetic analysis and CC can be used for raising antibodies for experimental, diagnostic and CC can be used for raising antibodies for experimental, diagnostic and CC can be used for raising antibodies for experimental, diagnostic and CC carays for diagnostics (which may be used to determine function of an CC encoded protein); and to detect differences in expression levels between CC diagnostic, e.g. to identify abnormal or diseased tissue in a human, to CC concer). The polynucleotides or susceptibility to a disease such as CC cancer). The prognosis and management of colorectal cancer, breast cancer, cc and lung cancer. The polynucleotides can also be used to screen for cc peptide analogues and antagonists.
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Jones WL. Kassam A. Kennedy GC. Kita D. Labat I;
Lamson G. Leshkowitz D. Pot D. Randazzo F. Reinhard
Stache-Crain B. Sudduth-Klinger J. Williams LT;
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ALIGNMENTS

	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX201324	RESULT 1
Hillan, K.J., Marsters, S.A., Pan, J., Pitti, R.M., Roy, M.A., Smith, V., Stone, D.M., Watanabe, C.K. and Wood, W.I.	Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,	1 (bases 1 to 1353)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	·	AX201324.1 GI:15391154	AX201324	Sequence 3 from Patent WO0153486.	AX201324 1353 bp DNA linear PAT 30-AUG-2001		

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                                                                                                                        Direct Submission
Submitted (25-MAR
South San Francis
                                                                                                                                                      Ashkenazi,A.
                                                                                                                                                              Marsters, S.A.,
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                                                                                                                                                                                                                      Ashkenazi, A. Identification
                                                                                                                                                                                                                                      Marsters, S.A.,
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/function="binds to
Apo3/DR3"
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                                    /gene="APO3L"
58. .807
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/chromosome="17"
                                                                                                                          (25-MAR-1998)
Francisco, CA
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                                                                /map="17p13"
                                                                                                                Location/Qualifiers
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Sheridan, J
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(APO3L) mRNA,
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                    death-domain-containing
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/protesin_id="AAC39724.1"
/protesin_id="AAC39724.1"
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YYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLAL
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Bourdon, P., Hession, C.,
Direct Submission
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Hession,C., Garcia,I. and Browning,J.L.
TWEAK, a new secreted ligand in the tumor
                                                                                                                                                                                                                                                                                                                                                     Homo
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                                                                                                                                                                                                                                    J. Biol. Chem.
98070415
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                                                                                                                                                                Cambridge, MA 02142, USA
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/product="TWEAK"
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                                                                                                                                                   Location/Qualifiers
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                                                      CCCCACAGTCGTCCCAGGCTGCCGGCTCCCCTCGACAGCTCTCTGGGCACCCGGTCCCCT
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a 434 c 368 g 257 t
                 AGCCGCTCTTTGCTCCAGACCTGCCCCTCCCTCTAGAGGCTGCCTGG
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Pred. No. 2.1e-224;
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patent US 6207642.
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Homo sapiens, superfamily, maccomplete cds. BC019047
BC019047.1 GI
GI:17512138
                                  Similar to
                          12,
                          clone MGC:20669
                                          1651 bp
                                   necrosis
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                         linear PRI
factor (ligand)
IMAGE:4766071,
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                                    GGGGAGCCGGCACCGCCTGCTGGTCCCGCTCGCGCTGGGCCTGGGCCTGGCCTTGGCC
                                                                                                CAGGCACAGCCCCCCCCCCATGGCCCCCCTCGGAGCCAGAGGCGGAGGGGGGCGCCCGG
                                                                                                                                                                                    Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://image.lln Series: IRAL Plate: 30 Row: p Column: 5
This clone was selected for full length sequencing because passed the following selection criteria: matched mRNA gi: 4
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,r., Wetherby.K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley.R.W., Bouffard,G.G., Brinkley.C., Brooks,S.,
Benjamin,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Mastello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Arrayed by: 1
DNA Sequencing by: Nationa
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
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immalia; Eutheria; Primates; Catarrhini; Hominidae;
(bases 1 to 1651)
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superfamily, member 12"
/protein_id="AaH190471"
/db_xref="GI:17512139"
/db_xref="GI:17512139"
/translation="MAARRSQRRRGRRGEPGTALLVPLALGLGLALACLGLLLAVVSL
GSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTR
ARRAIAAHYEVHPRPGQDGAQADGGYTTCLRP"
a 517 c 481 g 309 t
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/db_xref="taxon:9606"
/clone="MGC:20669 IMAGE:4766071"
/tissue_type="Primary B-Cells fro
/clone_lib="NIH_MGC_48"
/lab_host="DH10B-R"_
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Pred. No. 4.1e-190;
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AL Submitted (OB DEC-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

223 (bases 1 to 177703)

23 (bases 1 to 177703)

24 Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choppel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kalls, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Naguen, C., Nicol, R., Norbu, C., Norman, C.H., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Seaman, S., Severy, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Barown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferrestra, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Leu, C., Locke, K., Macdonald, P., Marquis, N., Klein, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
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Birren,B., Nusbaum,C. and Lander,E.
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ATCCGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCCTTCCTCACCTACTTCGGACTC
                                                                                                                                         GTGCTGGCCCTGCGCTGGAGGAATTCTCAGCCACTGCGGCGAGTTCCCTCGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 2, 2002 this sequence version replaced gi:15421989 All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79794 79893: gap of 100 bp 79894 99493: contig of 19600 bp in length 99494 99593: gap of 100 bp 99594 111049: contig of 11456 bp in length 111050 111149: gap of 100 bp 111150 125020: contig of 13871 bp in length 125021 125120: gap of 100 bp 125121 145100: gap of 100 bp 125121 145109: contig of 1989 bp in length 145210 169458: contig of 24249 bp in length 160450 160558.
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: Project Information
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48746 58277: cont:
58278 58377: gap of
58378 65804: cont:
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Center clone name: 186_B_7
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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45967 c 46568 g 41254 t 1
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177703: contig of 8145
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48745: gap of 100 bp
58277: contig of 9532 bp in length
58377: gap of 100 bp
65804: contig of 7427 bp in length
65904: gap of 100 bp
79793: contig of 13889 bp in length
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                                                                                                                                                                                                                                                                                                                                               56.0%;
99.6%;
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                                                                                                                                                                                                                                                                                                                         Score 768.2; DB 2; Pred. No. 2.4e-130; 0; Mismatches 3;
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Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Gupta,J.,
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Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
Marguiles,E.H., Masiello,C., Maskeri,B., Mastrian,S.D.,
McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R.,
Portnoy,M.E., Prasad,A., Schueler,M.G., Stantripop,S., Thomas,J.W.,
Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases 1 to 215795)
                                Submitted (17-JUL-2002) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA
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AC127470.1
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Center: NIH Intramural
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RP43-145D13,
Sequencing Center
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                                                                                                                                                                                                                                                                                                        30251
39213
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Contact: nisc_zoo@nhgri.nih.gov
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24776
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39312: gap of
4942: contig
4942: contig
60956: contig
60956: gap of
74520: contig
74620: gap of
74620: gap of
10557: contig
89522: contig
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rganism="Mus musculus" b_xref="taxon:10090" ell_type="peritoneal macrophages"679
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ORGANISM Mus musculus Description Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus REFERENCE 1 (bases 1 to 1168) AUTHORS Chicheportiche,Y., Bourdon,P.R., Xu,H., Hsu,Y.M., Scott,H., Hession,C., Garcia,I. and Browning,J.L. TITLE TWEAK, a new secreted ligand in the tumor necrosis factor family that weakly induces apoptosis JOURNAL J. Biol. Chem. 272 (51), 32401-32410 (1997) MEDLINE 98070415
9 00 AF03 TION MUS ION AF03 N AF03
QY 832 TTCGGACTCTTCCAGGTTCACTGAGGGGCCCTGG 865
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                                 AC126921
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AC126921.1 GI:21
HTG; HTGS_PHASE1;
                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (10-JUL-2002) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 153553)
Akhter, N., Antonellis, A.,
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                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: ddi

Center clone name: 045124
Center clone name: 045024
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 147046 bases at least Q30
Consensus quality: 147748 bases at least Q30
Consensus quality: 148024 bases at least Q20
Insert size: 15100; agarose-fp
Insert size: 15243; sum-of-contigs
Quality coverage: 8.72x in Q20 bases; agarose-fp
Quality coverage: 8.72x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: NIH Intramural Center code: NISC
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Eutheria;
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2412: gap of u

5841: contig o

5941: gap of u

6535: contig c

8535: contig c

8535: gap of u

15799: contig c
 25224:
25324:
32504:
32604:
41070:
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56590:
56690:
73769:
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                              gap of contig gap of contig
                              g of 15520 bp in
f unknown length
g of 17079 bp in
                                                         f unknown length
g of 8366 bp in le
f unknown length
g of 15520 bp in
                                                                                                                       unknown
of 7180
   unknown of 16990
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of 2494 bp in
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of 3429 bp
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111428: contig of 20469 bp in length
111528: gap of unknown length
15353: contig of 42025 bp in length
Location/Qualifiers
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41071, .56590
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/db_xref="taxon:9913"
/clone="RP42-45D24"
/clone_lib="RP42"
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TITLE
JOURNAL
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AUTHORS
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SOURCE
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Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,
Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R.,
Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,
Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Williamson, Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
World, W. R., Gibbs, S., Scherer, S., Sodergren, E., Weinstock, G.,
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                                                                                                                                             Submitted (31-MAY-2000) Human Genome Sequencing Center, Departed Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Jun 25, 2001 this sequence version replaced gi:12621364.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Mus musculus chromosome 11 clone SEQUENCE, 7 unordered pieces.
                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                         Worley, K.C.
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HTG; HTGS_PHASE1; HTGS_DI
                                                                                                                                                                                                                                                                                                   Unpublished
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               Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                               (bases 1 to 203083)
Center project Information
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3 DRAFT
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BASE COUNT
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                                                                                                                   TTCCAGGTTCACTGAGGGGCCCTGGTCTCCCCACAGTCGTCCCAGGCTGCCGGCTCC---
                                                                                                                                                                                                                                  ATCCGCACCCTCCCCTGGGCCCCATCTCAAGGCTGCCCCCTTCCTCACCTACTTCGGACTC
                                                                                                                                                                                                                                                                                                         CAGCTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGG
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                 --CCTCGACAGCTCTCTGGGCACCCGGTCCCTCTGCCCCCAGCCCTCAGCCGCTCTTTGCT
                                                                                                                                                                                                                                                                                 CAGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGGTCTTCCCTTCGG
                                                                                                                                                                                                                                                                                                                                                                            GTGCTGGCCCTGCGCTGCAAGAATTCTCAGCCACAGCAGCAAGCTCTCCTGGGCCC
AGCATCACCACACCTCCCTACCCCACCCCCACTCCTCCACCCCCTC-GCTGCTTCGGT
                                                                                        TTTCAAGTTCACTGAGGGGCCTTGCTCTCCCAGATTCCTTAAACTTTCCCTGGCTCCAGG
                                                                                                                                                                                      ATCCGCACCCTCCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTACTTTGGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. The true order of the pieces

is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemistry: Dye-primer Bodipy: 48% of reads
Chemistry: Dye-terminator Big Dye: 52% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 212648 bases at least Q40
Consensus quality: 218902 bases at least Q30
Consensus quality: 222384 bases at least Q30
Estimated insert size: 210656; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 7.2x in Q20 bases; sum-of-contigs estimation
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62253
118773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP23-168P5"
49293 c 47892 g
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62252: gap of unknown 1
118772: contig of 56520
118872: gap of unknown 1
148924: contig of 30052
149024: contig of 18207
167231: contig of 18207
167231: gap of unknown 1
187231: gap of unknown 1
196637: gap of unknown 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 309.6; DB 2;
Pred. No. 9.5e-47;
0; Mismatches 149;
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of 6530 bp in length
unknown length
of 6446 bp in length
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unknown length
of 56520 bp in length
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of 22576 bp in length
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of 30052 bp in
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                                                                                                                                                                                                                    only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Nov 20, 2001 this sequence version replaced gi:16605765. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                       http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-422L16 from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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AC119115
Rattus norvegicus
***, 32 unordered
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/note="Sequence from uni-directional primer reads and
big dye terminator reads only."
1 56824 c 57519 g 60529 t
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/db_xref="taxon:10090"
/chromosome="11"
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Direct Submission

Submitted (18-JUL-2002) Human Genome Sequencing Center, Departing to the Medicine, Departing the Medicine Departing 
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Direct Submitssion
Direct Submitssion
Submitted (25-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases_1 to 138792)
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2 (bases 1
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                               Center project Information Center project name: GUXG Center clone name: CH230-320N23
                                                                                         web site: http://www.hgsc.bcm.tmc.
Contact: hgsc-help@bcm.tmc.edu
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft" sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the filished sequence as the sequence of the
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Consensus quality: 112720 bases at least Q40 Consensus quality: 116666 bases at least Q30 Consensus quality: 119165 bases at least Q30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACI30192 177555 bp DNA linear HTG 08-AUG-200 Sus scrofa clone RP44-436K21, WORKING DRAFT SEQUENCE, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-AUG-2002) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA
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Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Consensus quality: 164120 bases at least Q40 consensus quality: 168085 bases at least Q20 consensus quality: 170767 bases at least Q20 Insert size: 169000; agarose-fp Insert size: 169000; agarose-fp Quality coverage: 4.78x in Q20 bases; agarose-fp Quality coverage: 4.78x in Q20 bases; sum-of-contigs
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Contact: nisc_zoo@nhgri.nih.gov
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3560: gap of unknown length
6869: contig of 3309 bp in length
6969: gap of unknown length
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                                                                                                  gap of unknown length contig of 11235 bp in
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                                                          gap of unknown length contig of 13570 bp in
                                                                                                                                                                                                                    contig of 6496 bp in length
of 17846 bp in
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45155. .58724
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13566. .21301
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115266. .177555
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/db_xref="taxon:9823"
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115265: gap of unknown length
177555: contig of 62290 bp in
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85.6%;
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RP81-332E11,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-O., Legaspi, R., Maduro, O.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. Insulative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-JUL-2002) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Green, E
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Akhter, N., Antonellis, A.,
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Mammalia; I
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                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: cwp
Center clone name: 33.E11
Center clone name: 33.E11
Center clone name: 33.E11
Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 148712 bases at least 040
Consensus quality: 151471 bases at least 030
Consensus quality: 153125 bases at least 020
Insert size: 152000; agarose-fp
Insert size: 16028; sum-of-contigs
Quality coverage: 5.36x in 020 bases; agarose-fp
Quality coverage: 5.10x in 020 bases; sum-of-contigs
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w. Rouffard,G.G., Breen,K., Brinkley,C.,
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              901 CGACAGCTCTCTGGGCACCCGGTCCCCTCTGCCCCACCCTCAGCCGCTCTTTGCTCCAGA 960
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                                               ATCCGCACCCTCCCCTGGGCCCCATCTCAAGGCTGCCCCCTTCCTCACCTACTTCGGACTC
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131786. .161428
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6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_phage:*
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11: sp_rodent:
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        09v5g2 drosophila
08xqx3 ralstonia s
09a926 caulobacter
09huw2 pseudomonas
09vfd4 drosophila
090vfd4 drosophila
090vf62 drosophila
066760 equine morb
016727 homo sapien
09uq01 homo sapien
09y556 homo sapien
09y556 homo sapien
09ft58 homo sapien
09ft58 homo sapien
09ft58 homo sapien
Q9ftn7
Q9aa15
Q9hur8
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ALIGNMENTS

QSYSG2 PRELIMINARY; PRT; 325 AA. AC QSYSG2 PRELIMINARY; PRT; 11, Created) DT 01-MAY-2000 (TrEMBLrel. 13, Created) DT 01-MAY-2000 (TrEMBLrel. 17, Last annotation update) DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) DT CG12919; CG12919 CG12919 CD EURATYCUTA; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; CR EURATYCUTA; CG12919 CD EURATYCUTA; CG12919 CG1291 CG1291 CG1291 CG1291
PRELIMINARY; PRT; 325 AA. 2975G2; 2975G2; 201-MAY-2000 (TrEMBLrel. 13, Created) 201-MAY-2000 (TrEMBLrel. 13, Last sequence update) 201-JUN-2001 (TrEMBLrel. 17, Last annotation update) 201-JUN-2001 (TrEMBLrel. 17, Last annotation update) 2012919 protein. 2012919 protein. 2012919, Last annotation update) 2012919, Last annotation update) 2012919, Last annotation update) 2012919, Last annotation update) 2012919, Last annotation update 2012919, L
update) update) update) Brachycera; Muscomorpha; Brachycera; Muscomorpha; Brachycera; Muscomorpha; Ins R.A., Golle R.F., Ins R.A., Galle R.F., Ins R.A., Galle R.F., Ing O., Chen L.X., In Beasley E.M., I.B., Boavies P., I.B., Davies

pseudomonas

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RA Merkulov G., Milshina N.V., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syler E., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-ry, Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Mysrs E.W., Rubin G.M., Venter J.C.;
RT Gibbs R.A., Mysrs E.W., Rubin G.M., Venter J.C.;
Science 287:2185-2195(2000)
DR EMBL: AE003831 AAF58484 ]; -
DR Flybase; FBgn0033483; CG12919.
DR InterPro: IPR000478; TNF fam****
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Best Local
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MEDLINE=21681879; PubMed=11823852;

Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

Arlat M., Billault A., Brottler P., Camus J.C., Cattolico L.,

Arlat M., Billault A., Claudel-Renard C., Cunnac S., Demange
Chandler M., Choisne N., Claudel-Renard C., Saurin W., Schiex T.
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SMART; SMO0207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
PROSITE; PS50049; TNF_2; 1.
                                                                                  Gaspin C., Lavie M., Moisan A., Rob
Siguier P., Thebault P., Whalen M.,
Weissenbach J., Boucher C.A.;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-GMI1000;
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O1-MAR-2002 (TrEMBLrel. 20, Created)
O1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable activation/secretion signal peptide prot.
RSP1055 OR RS02601.
                                "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid megaplasmid.
Bacteria; Proteobacteria;
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SMART; SM00207; TNF; 1.
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Q9A926;
                                                                                                                                                                                                                                      Nierman W.C., Feidblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O. Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid; Complete proteome. SEQUENCE 557 AA; 60786 MW;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; PubMed-11259647;
                                                                                                                                                                                                    Hypothetical protein; Complete SEQUENCE 210 AA; 22344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Caulobacter
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
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149
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                                                                                                                 2 LSLGLALACLGLLLVVVSLGSWATLS-AQEPSQEELTAEDRREPPE--LNPQTEESQDVV 58
                        SPLRYD
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EGFDFD
                                                                                                   LRLGLAVFAAGVAATVIVQAAWRSLASSKLQTQAATAPLVLDKPRF---TGVLKDGRPFL
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62; Conserv
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rel. 20,
rel. 20,
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                                                                                                                                                                7.8%;
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Last
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Pred. No. 2;
25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                  Pred. No. 1.1;
9; Mismatches
                                                                                                                                                                   Score 90.5;
Pred. No. 1
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8B9830ADFBF7F45C
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No. 2;
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Best Local S
Matches 53
SEQUENCE:
STRAIN-BERKELEY;
STRAIN-BERKELEY;
MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R., Ananatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson George R.A., Levis S.E., Richards S., Ashburner M., Henderson Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer
                                                                                                                                                                                                                                                                                                                                                                                                                      09VFD4;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2000 (TrEMBLrel. 1
CG18442 protein.
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09ниw2;
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                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004898; AAG08236.1;
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01-MAR-2001 (TrEMBLrel.
01-OCT-2001 (TrEMBLrel.
Hypothetical protein PA4
                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                    CG18442
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13,
14,
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Last sequence update)
Last annotation updat
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Pred. No. 2.7;
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                                                                             ayne J.D.,
, Galle R.F.,
                                                Pfeiffer B.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
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RESULT 6
Q90WT9
ID Q90W
AC Q90W
AC Q90W
AC Q1-D
DT 01-D
DT 01-M
DE TNFCS Gall
OC Euka
CC Arch
OC AC
OC ACC

Q90WT9

PRELIMINARY;

287 À

SEQUENCE FROM NCBI_TaxID=9031; Archosauria;

Aves;

Neognathae;

Chordata; Craniata; Vertebrata;

Galliformes;

Phasianidae;

Phasianinae;

Euteleostomi;

O90WT9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
TNF-related apoptosis inducing ligand.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat.

update)

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QΥ
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В
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Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.M.,
RA
Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.M.,
RA
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Durker B.C., Dunk D.,
RA
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA
FOSIer C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA
Glodek A., Gong F., Gorrell J.H., Gu Z., Kennison J.A., Ketchum K.A.,
RA
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA
Harris N.L., Ralush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA
Liu X., Mattel B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA
Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPharson D.
RA
McIntolvo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA
Alason D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA
Yeb J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A.,
RA
Allims S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA
Alman S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA
Alman S.M., Woodage T., Worley K.C., Wu D., Smith H.O.,
RA
Schence 287:2185-2195(2000).
DR
EMBL, RAD03707; AAF55126.1; -
RA
Schence 287:2185-2195(2000).
DR
EMBL, RAD03707; AAF55126.1; -
RA
Schence S. Bota A.; 86321 MW; FDF9EFEF14E69957 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C. Ballew R.M., Baxu A., Baxendale J., Bayraktaroglu L., E Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bols
642
                                          144
                                                                                   590
                                                                                                                             116
                                                                                                                                                                                                                                                           482
                                                                                                                                                                      530 PVMQPQERRELCPPQLPPRGSPTLDGSQSSPTNAVSGPKKPPLPPIACRPRPSNGVNSPN
                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                      29
HLIDGEALLAKTDVAMSGLLIKLDQVAAQC----SVAQAAGGGTSI
                                        HFDEGKAVYLKLDLLVNGVL-----ALRCLEEFSATAASSPGPQL
                                                                                                                           SSS-----PLRYDRQI-----
                                                                                                                                                                                                                   YEVHPR----
                                                                                                                                                                                                                                                           EQPGQEEL-----QPPPRTPTTEQ-----LSPPPARPPKSAELLQRYSPKKQVRIAAS 529
                                                                                                                                                                                                                                                                                                    QEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKGRKARPRR--AIAAH 86
                                                                                   SSSPGSAPPAHYSPPIPATVRLPHLNQANGTLPLLPKKPQQLHGEKLFIKNG--
                                                                                                                                                                                                                                                                                                                                              l Similarity
49; Conser
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                              7.78;
21.78;
                                                                                                                                                                                                                -PGQDGAQAGVDGTVSGWEETKI---
                                                                                                                                                                                                                                                                                                                                              27;
                                                                                                                                                                                                                                                                                                                                        Pred. No. 7.7;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    Score 89.5;
                                                                                                                                                                                                                                                                                                                                                                                       DB 5;
                                                                                                                             ----GEFTVIRAGLYYLYCQV
                                                                                                                                                                                                                                                                                                                                              55;
                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                              Indels
683
                                          183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chandra I.,
                                                                                                                                                                                                                                                                                                                                              95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G.L.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        н.
                                                                                                                                                                                                                --N 115
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K.A.,
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RESULT OF SOLUTION OF SOLUTION
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    Matches
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Best Local
                                                                                                                                                      Wang L.-F., Yu M., Pritchard L
Submitted (JUN-2000) to the EM
EMBL; AF017149; AAC83191 1; -
InterPro; IPR000982; Matrix.
                                                                                                                                                                                                                                                                                                         Wang L.F., Yu M., Hansson E., Pritchard L.I., Shi
Michalski W.P., Eaton B.T.;
"The exceptionally large genome of Hendra virus:
of a new genus within the family Paramyxoviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yu M., Hansson E., Langedijk J.P., Eaton B.T., Wang L.F.; "The attachment protein of Hendra virus has high structural but limited primary sequence homology compared with viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD002012; TNF_abc; 1. PROSITE; PS50049; TNF_2; 1. SEQUENCE 287 AA; 32092 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (OCT-2001)
EMBL; AY057941; AAL2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ovary."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bridgham J.T
"TNF-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             but limited primary sequence denus Paramyxovirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA negative-strand vi.
Paramyxoviridae; Paramyxovirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                089341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  089341
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                                                                                                                                 Pfam; PF00661; Matrix; 1.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20481636; PubMed=11024125;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99058172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-63330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hendra virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 AAHYEVHPR-PGQDGAQAGVDG-----TVSGWEETKINSS-SPLRYDRQIGEFTVIRA 134
                         Local
                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASSPGPQ--LRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CWAPEAEYGLHALYQGGLFELKAGDELFVSVSSLAIDYSDAAASYFGAFRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLYYLYCQVHFD-------EGKAVYLKLDLLVNGVLALRCLEEFSATA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAHLIFRPQNPAQDGSSRRFGNLSQSCRHAITRWEDSTIHSHLQNITY--RDGRLRVNQA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKYYVYSQIYFRYSRDGAGARVSVPQLVQCINWKTSYSQPILLLKGV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paramyxovirus.";
ogy 251:227-233(1998).
    Similarity
39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                                                                                                             PD000741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                         74:9972-9979(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis
                                                                                          A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAL23702.1;
                                                                                        Matrix; 1.
; 39793 MW;
                                                                                                                                                                                                                       Pritchard L.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.78;
                         7.7%;
28.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inducing
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19,
    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
Score 89; DB Pred. No. 3; Nismatches
                                                                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 89;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 viruses; Mononegavirales;
he; Morbillivirus.
                                                                                          79E238DE496828D5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB06E1C95087B108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligand (TRAIL) expression
                                                                                                                                                                                                                       Hansson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB
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                                             12;
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    50;
                                                                                                                                                                                                                                                                                                                                                                              Shiell
                                                                                                                                                                                                     databases
                                                                                                                                                                                                                       Eaton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                        CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
                                           Length 352
                                                                                                                                                                                                                                                                                                                support for .";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
    Indels
                                                                                                                                                                                                                       B.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in the hen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity
                                                                                                                                                                                                                                                                                                                                  creation
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S

78

RPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRAGLY 137

Query Match

Score

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                                                                                                                         RA Adams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Berson R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.C.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.C.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Durbin K.J., Evangelista C.G., Ferraz C., Ferriera S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Haris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Weinstend M.P., Ketchum K.A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mentan J., Welson K.A., Nixon K., Nusskern D.R., Pacles J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Weisen D.R., Welson K.A., Nixon K., Nusskern D.R., Pacles J.M.,
RA Weisen C., Siden-Klamos I., Simpson M., Skupski M.P., Saith T.,
RA Rander E., Sentha D.A., Weissenbach J.,

                                                        Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
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01-MAY-2000
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    AE003813; AAF58200.1;
se; FBgn0033970; CG102
NCE 224 AA; 25025 M
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Neoptera; Endopterygo
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Drosophilidae; Drosophila.
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      780B9EF7BBAFF156 CRC64;
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Matches

13

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Best

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Query Match
Best Local
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EMBL; U49404; AAB39504.1; -.
InterPro; IPRO00982; Matrix.
Pfam; PF00661; Matrix; 1.
ProDom; PD000741; Matrix; 1.
SEQUENCE 353 AA; 40142 MW;
                                                      01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update Placental-like alkaline phosphatase precursor (EC
                                                                                                                           Q16727 PRELIMINARY
Q16727;
Q1-NOV-1996 (TrEMBLrel.
Homo sapiens (Human).
Eukaryota; Metazoa; (
Mammalia; Eutheria; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-96419932; Pubmed-8822631;
Gould A.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Morbillivirus.
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Equine morbillivirus
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                                                                                                                                                                                                                                                                            FSLMDINPW----LNRLTW
                                                                                                                                                                                                                                                                                                                   SGLLPLRPGSSLRIRTLPW
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                                                                                                                                                                        PRELIMINARY;
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28.1%; Pre
    Primates;
                         Chordata;
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7; Mismatches
  Craniata; Ve
Catarrhini;
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3.7;
                       Vertebrata; Euteleostomi;
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    Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 353;
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Q9UQ01
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AC Q9UQ0
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EXALACT
GN KIAACT
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Q9UQ01;
Q1-MAY-2000 (TYEMBLTel. 13, C:
Q1-MAY-2000 (TYEMBLTel. 13, L
Q1-DEC-2001 (TYEMBLTel. 19, L
KIAA0929 protein (Fragment).
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Gum J.R., Hicks J.W., Sack T.L., Kim Y.S.;
"Molecular Cloning of Complentary DNAs Encodi
in Human Colon Cancer Cells.";
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EMBL; X53779; CAA37374.1; -.
HSSP; P00634; 1AJC.
InterPro; IPR001952; Alk_phosphtse.
Pfam; PF00245; alk_phosphtse.
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SIGNAL
CHAIN
    1400
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Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,
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The complete sequences of 100 new cDNA clones from brain which co
for large proteins in vitro.";
DNA Res. 6:63-70(1999).
DNA Res. 6:63-70(1999).
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HOmo sapiens (Human).

Homo sapiens (Human).

Chordata;

Chordata;

Choria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00113; ALKPHPHTASE.
ProDom; PD001868; Alk_phosphtse; 1.
SMART; SM00098; alkPPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-COLON;
                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 --- TAASSPGPQLRLCQVSGLLPLRPGSSLRIRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130
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    QPRLPAGPANRPPEPHTQVQRAQAETGPTSFPSPVSVSMKPDL-PVSLPTQTAPKQPLFV 1458
                                           QEELTAEDRREPPELNPQTEESQ------DVVPFLEQLVRPRRSAPK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGV-----LALRCLEEFSA-----
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                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1
20
532 AA;
                                                                                                                                                                      1663 AA;
                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19
532
57399 MW;
                                                                                                     7.6%;
                                                                                                                                                                      173871 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.6%;
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                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 88; DB Pred. No. 6.3; l6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                         Score
Pred.
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PLACENTAL-LIKE ALKALINE PHOSPHATASE

354B345CB19A0BC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- LVHGVQEQTFIAHVMAFAACLEPYTACDLAPS
                                                                                    Mismatches
                                                                                                                                                                      EC94D17086A8531E CRC64;
                                                                                                         No.
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27;
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                                                                                                                                                                                                                                                                         from brain which code
                                                                                                                         Length 1663;
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                                                                                                                                                     01-DEC-2001
01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                     Q96T58;
Q96T58;
                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                            SHARP
                                                                                                                                                                                                                                                                                                                                                         3147
                                                                                                                                                                                                                                                                                                                                                                                                                                             3104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhodes S., Huckle E.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ EMBL; AL096858; CAB51072.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical 357.0 kDa protein. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1549
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NCBI_TaxID-9606;
                                                                                                                               Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00360; RRM; 2.
PROSITE; PS50102; RRM; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPRLPAGPANRPPEPHTQVQRAQAETGPTSFPSPVSVSMKPDL-PVSLPTQTAPKQPLFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTTSGPSTPPGLVLPHTEFQPAPKQDSS-----PHLTSQRPVDMVQLLKKYP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00076; rrm; 2.
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42; Conserv
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                                                                                                                          (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
aptor transcription cofactor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                              PRELIMINARY;
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Primates;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Catarrhini; Hominidae;
                                        Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F8BB6A645DD9B6BC CRC64;
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                                                               Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вg
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                                           Hominidae;
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                                                                 Euteleostomi;
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Best Local S
                                                                                                            Matches
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Hon M., Evans R.M.;
"SHARP, an inducible cofactor t
repression and activation.";
Genes Dev. 0:0-0(2001).
EMBL; AF356524; AAK52750.1;
                                                                                                                                                                                                              STRAIN-CV. NIPPONBAKE; Sasaki T., Matsumoto T., Yaman "Oryza Sativa nipponbare(GA3)
                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Liliopside
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3401
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                    Putative ReriA protein (AtRERIA). P0005A05.12.
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                                                                                                                                                        InterPro; IPR004932; Rerl. Pfam; PF03248; Rerl; 1. SEQUENCE 522 AA; 58171
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                          Q9FTN7;
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Pfam; PF00076; rrm; 4
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                                                                SSSKGREGFAAREVVA----SPSGFRPGFSMDGAADSGTAGAAAAAAKWRTDASRAFQYY 256
                                                                                      SAPKGRKARPRRAIAAHYEVHP---RPG--QDGA----QAGVDGTVSGWE-----ETK 113
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                     LDRSTPHATGRWIGTLAV--AAIYAL--RVYLVQGFYIVTYGLGIYL-LNLLI-GFLSPM
                                         INSSSPLRYDRQIGEFTVIRAGLYYLYCQVHFDE-----GKAVYLKLDLLVNGVLALR 166
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                                                                                                           Score 87.5; DI
Pred. No. 6.9;
21; Mismatches
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Pred. No.
                                                                                                                                                                                                                       genomic DNA, chromosome 1,
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annotation
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Search completed: March 31, 2003, 07:46:15 Job time: 56.8782 secs
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Best Local Similarity
Matches 43; Conserv
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Alpha-glucosidase, putative.
CCO796.
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MEDLINE-21173698; pubMed-11259647;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Vannathevan J., Ermolaeva M., White O.,

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

EMBL; AB005755; AAK22781.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 670 AA;
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Bacteria: Proteobacteria; alpha subdivision; Caulobacter group;
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                                                                                                                                                           611
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                                                                                                                                               GRTVKVPLSFLGNGAFSAEIREDGAEPTALKTRTQSVASKDTLTLKLAPGGGGVIRISP
                                                                                                                                                                                                                     GKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLLPLRPGSSLRIRTLP 206
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Command line parameters:

MODEL-frame+_p2n.model -DEV=x1h

-MODEL-frame+_p2n.model -DEV=x1h

-O-/cgn2_1/USPTO_Spool_US09245198/runat_24032003_163554_25956/app_guery.fasta_1.846

-OB-EST -QFWT-fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0

-UNITS-bits -START=1 -END=-1 -MARRIX=Dlosun62 -TRANS-human40.cdi -LIST=45

-DCCALIGN=200 -THR_SCORE-pot -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL

-OUTFWT-Pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAXLEN-2000000000

-USER-US09245198_6CGN_1_1_2463_@runat_24032003_163554_25956 -NCPU=6 -ICPU=3

-NO_XLPXY -NO_MMAP -LARGOUERY -NGS_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120

-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Fgapop 6.0 , 1
Delop 6.0 , 1
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1162
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

45	44	C 43	42	41	40	39	38	c 37	36	35	34	33	c 32	31	30	29	28	27	26	25	24	23	c 22	21	20	19	18	17	16	15	14	13	12	11	10	۰	ω ·	7	on .	σ.	4 (ادسا	2	<u>.</u>	Result No.
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B642326 BB6	824443 6030	Q208433 UI-R	966255 ie72	G110063 6022	uu30c03.	B596688 BB5966	906850 60306463	W320117 un17b0	967060 id27h07.	52313 ud87h02.	686319	55379 yj77a08.ı	073881 220949	7970 vr30al0	17023 52923	M688946 UI-E	MR1.	1738634 6033588	538	08274 603	E307031 601	1965174 id:	F466521 UI:	44430 BP	1509 BP	762908 603	654876 UI:	404836 603	21610 my18d09	0722	917574	74188	21213 AGENCOU	K020909 Mus	0671259 AGE	0884231 AGE	707185 AG	W763237 ur	1766766 603056	1596681 60324	1819200 603034	1870393 60339	1871711 603395	77781 602092	Description

ALIGNMENTS

MS	z	RESULT 1 BF577781 LOCUS BF577781 DEFINITION 6020920801
. Motagos. Chordata. Craniata. Vertebra	lence. 1 GI:11651493	BF577781 918 bp mRNA linear EST 12-DEC-2000 602092080F1 NCI CGAP CO24 Mus musculus cDNA clone IMAGE:4206595 5′,
tu. 5:+01000+034.		e IMAGE:4206595 5',
BUNGTYCHG. MICHAGOG, CHOTAGHA, CTAHTAGA, YATCACTACA, BACATACACOMI.	MSIN	NSIN SO NOI

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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9767 row: p column: 20
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Contact: Robert St
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/clone_lib="NGI_CGAP_CQ24"
/clone_lib="NGI_CGAP_CQ24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Best Local Similarity:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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Plate: LLAM12034 row: b column: 07
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Mammalia; Eutheria; Primates;
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/Clone_lib="NHL_MGC_90"
/Clone_lib="NHL_MGC_90"
/Lissue_type="adenocarionma, cell line"
/Lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."
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603395641F1 NIH_MGC_90 Homo
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                                                                                                         CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, )
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/db_xref="taxon:9606"
/clone="IMAGE:5405459"
/clone=Lib="NIH_MGC_90"
/clone_Lib="NIH_MGC_90"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6;
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Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

125 a 240 c 227 g 136 t
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US-09-245-198A-2 (1-225) x BI870393 LeuProTrpAlaHisLeuLysAlaAlaProPheLeuThrTyrPheGlyLeuPheGlnVal LeuCysGlnValSerGlyLeuLeuProLeuArgProGlySerSerLeuArgIleArgThr LeuArgCysLeuGluGluPheSerAlaThrAlaAlaSerSerProGlyProGlnLeuArg AlaHisTyrGluValHisProArgProGlyGlnAspGlyAlaGlnAlaGlyValAspGly 104 GTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAAACACGGGCTCGAAGAGCGATCGCA ValArgProArgArgSerAlaProLysGlyArgLysAlaArgProArgArgAlaIleAla TCGGAACTGAATCCCCAGACAGAAGAAAGCCAGGATCCTGCGCCTTTCCTGAACCGACTA ProGluLeuAsnProGlnThrGluGluSerGlnAspValValProPheLeuGluGlnLeu LeuSerAla---GlnGluProSerGlnGluGluLeuThrAlaGluAspArgArgGluPro CTCCCCTGGGCCCATCTCAAGGCTGC-CCCTTCCTCACCTACTTCGGACTCTTCCAGGTT CTCTGCCAGGTGTCTGGGCTGTTGGCCCCTGCGGCCAGGTCC-TCCCTGCGGATCCGCACC CTGCGCTGCCTGGAGGAATTCTCAGCCACTGCGGCCCAGTTCCCTCGGGCCCCAGCTCCGC CTGTCCGCCCAGCAGGAGCCTGCCCAGGAGGAGCTGGTGGCAGGAGGACCAGGACCCG BI819200 603034614F1 2.99e-89 941.50 91.86% 87.78% 81.02% NIH_MGC_115 Homo (1-728)Conservative: Mismatches: Indels: Gaps: Length: Matches: bp mr cDNA clone IMAGE:5175698 728 194 9 17 17 184 481 164 421 144 124 241 84 181 64 44 659 224 600 541 361 301 121 61 25 204 ű

GI:15930750

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                                                                                                                                                       AlaGlnAlaGlyValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSer
TACCTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTG
                                                                                                                                     GCGCAGGCAGGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCC
                                                                  AGCCCTCTGCGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, M
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
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/clone="IMAGE:5175698"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh
Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11722 row: k column: 13

High quality sequence stop: 776.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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1. (bases 1 to 828)
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                                                                                                                                                                                                                       /note="Organ: brain; Vector: pBluescriptk (modified pBluescript KS+); Site_1: BamHI; Site_2: SalTTTTTTTVN-3', 011go-dT primed using primer 5'-TTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched
                                                                                                                                            for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Li constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Lib 278 c 223 g 172 t
                                                                                                                                                                                                                                                                                                       /tissue_type="hypothalamus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:5285892"
/clone_lib="NIH_MGC_96"
                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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US-09-245-198A-2 (1-225) x BI596681 (1-828)

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                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11517 row: c column: 18
High quality sequence stop: 772.
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603056866F1 NIH_MGC_122
                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 834)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                                                                                                      quality sequence stop:
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5206217"
/clone_1ip="NIH_MGC_122"
/lab_host="DH10B"
                  /note="Organ:
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pooled lung and spleen; Vector:
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Homo
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sapiens cDNA clone IMAGE:5206217 5',
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Best Local Similarity
Query Match:
                                          VERSION
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AW763237.1 GI:7695174
                                                                                     ur70d09.yl NCI_CGAP_Mam3 similar to TR:054907 0549
Mus musculus
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                house mouse
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DNA clone IMAGE:3155633 5'
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Eukaryota;

Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

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GGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
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Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
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1 (bases 1 to 561)
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22, 37-43 (1999)."

158 c 194 g 100 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:3155633"
/clone_lib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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64 LeuValArgProArgArgSerAlaProLysGlyArgLysAlaArgProArgArgAlaIle

CCGTCGGAACTGAATCCCCAGACAGAAGANAGCCAGGATCCTGCGCCTTTCCTGAACCGA

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KEYWORDS
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Dr. Mark Watson
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /Clone_Tiba"NIH_MGC_113"
/clone_liba"NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTBP; Site_1: XhoI; Site_2:
/note="Organ: spleen; Vector: pOTBP; Site_1: XhoI; Site_1: Xho
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/db_xref="taxon:9606"
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AGENCOURT_8682031 Lupski_sciatic_nerve Homo
IMAGE:6197488 5', mRNA sequence.
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National Institutes of Health, Mammalian
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                                                                                  /organism="Homo sapiens"
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/clone="IMAGE:6197488"
/clone_lib="Lupski_sciatic_nerve"
                                                                    /sex="male"
/note="Vector: pCMV-SPORT6 (Life Technologies);
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US-09-245-198A-2 (1-225) x BQ884231 (1-940)
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Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Blos.A.G.E. Corporation
Clone distribution: MGC clone distribution information can
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/lab_host="DHIUB (phage-resistant)"
/note="organ: sallvary gland: Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
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RS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arrakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Nardon, M., Rodriguez, I., Sakamoto, N., Saski, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Sand, K.S., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., and Havashiraki, Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Havashiraki, Y.
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Mus musculus (strain:C57BL/6J) adult clone_lib:RIKEN full-length enriched
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High-efficiency full-length cDNA
Meth. Enzymol. 303, 19-44 (1999)
Nature 409 (6821),
21085660
                                  Functional annotation of a full-length mouse Nature 409 (6821), 685-690 (2001)
                                                                                                                    and Hayashizaki,Y
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiranoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishi, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Ouackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Soqaba, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B. Retina RNA was provided by Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurobiology, Harvard Medical School, 220 Longwood Ave., Boston, MA 02115, USA) whose assistance is gratefully acknowledged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gratefully acknowledged.
Retina RNA was provided by Stefano Gustincich (Department of
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                                                                                                                                                           tumor necrosis factor (ligand) superfamily, member 12"
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5', mRA sequence.
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B0674188.1 GI:21785022
  Eukaryota; Metazoa;
Mammalia; Eutheria;
                          Homo sapiens
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              LeuCysGlnValSerGlyLeuLeuProLeuArg-ProGlySerSerLeuArgIleArgTh
                                                                         CTGCGCTGCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGGGCCCAGCTCCGC
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National Institutes of Health, Mammalian Gene
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: ATCC
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Plate: LLCM2459 row: d column:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."

a 286 c 315 g 184 t 1 others
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                                                                                                                                                   GAGACCAAAATCAACAGCTCCAGCCCTCTGCGCTATGACCGCCAGATTGGGGAATTTACG
                                                                                                                                                                                                              Email: nhlee@tigr.org
This clone is available through the ATCC,
tel#703-365-2700 for further information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Institute for Genomic Research 9712, Medical Center Drive, Rockvi. Tel: (301)-838-3529
Fax: (301)-838-0208
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EST34878 Rat gene index, normalized
Rattus norvegicus cDNA clone RGIEF49
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                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2
Xho1; Estimated insert size approx.1 kb"
188 c 147 g 138 t 3 others
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Bento Soares"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus norvegicus
/db_xref="taxon:10116"
/clone="RGIEF49"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="mix - brain, ovary, placenta,
liver, embryo, heart, muscle, spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="SOLR"
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Rodentia;
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 445)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu, Marra, M., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA870722
445 bp mRNA 1:
vq25g07.rl Barstead stromal cell line MPLRB8
clone IMAGE:1095324 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:601556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 house mouse
                                                                                                                                   102
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                                                                                                                                  Library constructed by Bob Barstead. The C2C12 ce (available from ATCC, catalog # CRL-1772) different rapidly, forming contractile myotubes and producing characteristic muscle proteins.
                                                                                                                                                                                                      /clone="IMAGE:1095324"
/clone_lib="Barstead stromal cell line
                                                                                                                                                                                                                                                                                                                            /cell_line="C2C12 (undifferentiated)
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
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               Conservative: Mismatches: Indels:
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Search completed: March 31, 2003, 05:25:11 Job time: 1507.86 secs

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Gapop 10.0 ,
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1 VLSLGLALACLGLLLVVVSL......PWAHLKAAPFLTYFGLFQVH
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    Query
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TNF6_RAT
TNI3_MOUSE
TNFC_MACEU
PPB2_HUMAN
PPB1_HUMAN
PPB1_HUMAN
PPB3_HUMAN
PPB3_RAT
TNFB_RABIT
TNFB_RABIT
TNFB_RABIT
TNFB_RABIT
TNFB_HUMAN
TNF5_FELCA
PHVD_ARATH
T13B_HUMAN
APP2_HUMAN
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TNI1_RAT
PPBN_HUMAN
TNEC_HUMAN
TNES_AOTTR
TNES_CALJA
TNIS_CALJA
TNI4_HUMAN
TNIS_CALJA
TNI4_HUMAN
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7 macropus eu
1 homo sapien
7 homo sapien
8 homo sapien
8 mus musculu
7 rattus norv
4 oryctolagus
7 synechocyst
6 caenorhabdi
1 homo sapien
5 felis silve
7 arabidopsis
5 homo sapien
1 homo sapien
1 homo sapien
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7 macaca mula
7 macaca neme
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homo sapien
aotus trivi
callithrix
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8 gallus gall
5 m tumor nec
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TN12_MOUS
ID TN12
AC 0549
DT 15-.
DT 15-.
DT 15-.
DT 6-.
DT 15-.
DT 6-.
DT 15-.
DT 6-.
DT 70-.
TN 70-
    8888
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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TN12_MOUSE STANDARD; PRT; 225 AA. 054907; Q9CTP2; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member inducer of apoptosis) (TWEAK) (Fragment).
  <del>:</del> :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Peritoneal macrophage;
MEDLINE-980770415; PubMed-9405449;
Chicheportiche Y., Bourdon P.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFSF12.
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Result No.

ALIGNMENTS

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

12

(TNF-related weak

×u Η., Hsu

Y.-M.,

Scott H.,

-!- TISSUE SPECIFICITY: WIDELY EXPRESSED.	888
-!- SUBUNIT: Homotrimer (Potential)!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).	8888
inducer of apoptosis in some cert types, riomotes anglogenesis and the proliferation of endothelial cells. Mediates NF-KappaB artivation (By similarity)	388
reactive 409:607-690(2001). -i- FUNCTION: Binds to FN14 and possibly also to TNRFSF12/APO3. Weak	488
"Functional annotation of a full-length mouse cDNA collection.";	감감
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Havashizaki Y.:	R A
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,	RA
Nordone P., King B., Kingwald M., Kodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch KF.,	RA
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,	RA
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,	RA
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,	R A
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,	RA
Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,	RA
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,	RA ?
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Flatschmann W. Gasaterland T. Gissi C. King B. Kochiwa H.	R R A
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,	RA
	RA
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,	RA
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,	RA
MEDLINE=21085660; PubMed=11217851;	R :
STRAIN=C57BL/6J: TISSUE=Retina:	77 75
	RN
J. Biol. Chem. 272:32401-32410(1997).	RL
induces apoptosis.";	RΤ
"TWEAK, a new secreted ligand in the tumor necrosis factor family that	RT
Hession C., Garcia I., Browning J.L.;	RA

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TRESULT TRESUL
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                 TN12_HUMAN STANDARD; PRT; 249 AA. 0,43508; Q8WUZ7; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member inducer of apoptosis) (TWEAK) (APO3 ligand). TWEST12 OR ABO3L OR DR3LG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1196259; Tnfsf12.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
SEQUENCE FROM N.A., AND N-TERMINUS TISSUE-TOnsil, and Fetal liver; MEDLINE-98070415; PubMed-9405449; Chicheportiche Y., Bourdon P.R., XI
                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VLSLGLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPF
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SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEQLVRPRRSAPKGRKARPRRATAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPL
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69
167
115
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                                                                                                                                           (Human)
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BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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                                                                                                                       Chordata;
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TUMOR NECROSIS FACTOR LIGAND SUP
MEMBER 12, SECRETED FORM (BY SIM
SIGNAL-ANCHOR (TYPE-II MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1162; DB 1;
Pred. No. 4.3e-97;
                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90C412CC0480659B CRC64;
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   Ή.,
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                                                      SOLUBLE
   Hsu Y.-M.,
                                                                                                         Hominidae;
                                                      FORM
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ORM (BY SIMILARITY)
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                     CARBOHYD
                                                                      DOMAIN
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                                                                                                         TRANSMEM
                                                                                                                           DOMAIN
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249

MW:

249 94 139

EXTRACELLULAR (POTENTIAL) CLEAVAGE.

N-LINKED (GLCNAC.

E660843361C28EBA CRC64

1 22

21 42

CYTOPLASMIC (I

(POTENTIAL)

MEMBRANE

(POTENTIAL)

MEMBER 12, SECRETED FORM

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SMART; SM0020/; ...., FALSE_MEGG.

PROSITE; PS00251; TNF_1; FALSE_MEGG.

PROSITE; PS50049; TNF_2; 1.

Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.

Cytokine; Apoptosis; Transmembrane; Signal-anchor.

Cytokine; Apoptosis; Transmembrane; Signal-anchor.

Cytokine; Apoptosis; Transmembrane; Signal-anchor.

Cytoki
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MEDLINE-98228355; PubMed-9560343;
Marsters S.A., Sheridan J.P., Pit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entitles requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marsters S.A., S
Ashkenazi A.;
"Identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "TWEAK, a new secreted ligand in the "TWEAK, a new secreted ligand in the weakly induces apoptosis";
J. Biol. Chem. 272:32401-32410(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lynch C.N., Wang Y.C., Lund J.K., Chen Y.-W., Leal J.A., Wiley S.R.; "TWEAK induces anglogenesis and proliferation of endothelial cells."; J. Biol. Chem. 274:8455-8459(1999).

-i- FUNCTION: Binds to FN14 and possibly also to TNRFSF12/APO3. Weak inducer of apoptosis in some cell types. Mediates NF-KappaB activation. May promote anglogenesis and the proliferation of endothelial cells.
                                                                                                                                                                                                                                                       InterPro; IPR000478; T Pfam; PF00229; TNF; 1. SMART; SM00207; TNF; 1
                                                                                                                                                                                                                                                                                                                                                                         MIM; 602695;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lung and brain.
PTM: The soluble form
by proteolytic process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Type II membrane protein and somissue SPECIFICITY: Highly expressed in adult heart, skeletal muscle, brain, colon, small intestine, lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: Ref.3 sequence differs from frameshift in position 125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by proteolytic processing.

SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
SIMILARITY: Securence differs from that shown due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       skeletal muscle, brain colon, small intestine, lung, ovary, prostate, spleen, lymph node, appendix and peripheral blood lymphocytes. Low expression in kidney, testis, liver, placer thymnus and bone marrow. Also detected in fetal kidney, lives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMOTRIMER (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF055872;
BC019047;
                                                                                                                                                                                                                                                                                                                                                                                                        AF030099; AAC51923.1; AF055872; AAC39724.1; BC019047; AAH19047.1; AF0NC:11927; TNFSF12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          restrictions
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ing, ovary,
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TANDER RESULT TO SEE TO
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                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-White leghorn; TISSUE-Spleen;
A Tregaskes C.A., Young J.R., Burnside J.;
L Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
C. --- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).
C. --- SUBUNIT: Homotrimer (By similarity).
C. --- SUBCELULAR LOCATION: Type II membrane protein. Also exists as cextracellular soluble form (By similarity).
C. --- FTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
C. --- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local
                                  InterPro: IPR003263; TNF_5.
InterPro: IPR003636; TNF_abo.
InterPro: IPR00478; TNF_family.
InterPro: IPR00478; TNF_family.
InterPro: IPR00212; TNF; 1.
IPRODOM: PD002012; TNF_abc; 1.
IPRODOM: PD008600; TNF_5; 1.
SMART: SM00207; TNF; 1.
IPROSITE: PS00251; TNF_1; 1.
IPROSITE: PS00251; TNF_2; 1.
IPROSITE: PS0029; TNF_2; 1.
                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L) (CD154 protein)
TNFSF5 OR CD40LG O
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHICK
                       Cytokine;
                                                                                                                                                                                                       EMBL; AJ243435; CAB95748.1; HSSP; P29965; 1ALY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-2002 (Rel. 41, Last sequence update)
N-2002 (Rel. 41, Last annotation update)
necrosis factor ligand superfamily member
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 Transmembrane; Glycoprotein; Signal-anchor.
1 272 TUMOR NECROSIS FACTOR LIGAND
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Best Local :
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SEQUENCE
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                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                J. Biol.
                                                                                                                                                                   TRANCE is
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L.E.
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TN11_MOUSE STANDARD; PRT; 316 AA.

035235; 035306; Q9R1YO; Q9JJKB; Q9JJK9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
10-CT-2001 (Rel. 41, Last annotation update)
10-CT-2001 (Rel. 41, Last annotation update)
11-JUN-2002 (Rel. 41, Last sequence update)
11-JUN-2002 (Rel. 40, Created)
11-JUN-2002 (Rel. 40, Last sequence update)
11-JUN-2002
                                  TISSUE=Thymic lymphoma;
MEDLINE=98032977; PubMed=9367155;
Anderson D.M., Maraskovsky E., Bi
                                                                                                                                                                                                                                                                                                                                                     TISSUE-Hybridoma;
MEDLINE-97460112; PubMed-9312132;
Wong B.R., Rho J., Arron J., Robinson
Kalachikov S., Cayani E., Bartlett F.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFSF11 OR RANKL OR TRANCE OR OPGL.
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                                                                                                                                                                                                                    a novel ligand of the tumor ates c-Jun N-terminal kinase hem. 272:25190-25194(1997).
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   Roux E.R.,
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   Teepe M.C.,
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N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
5409F24A8E53CCD7 CRC64;
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Billingsley W.L., Dougall W.C., e M.C., DuBose R.F., Cosman D.,
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in T cells.";
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Boyle

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Yasuda H., Shima N., Nakagawa N., Yamaguchi K., Kinosaki Mochizuki S.-I., Tomoyasu A., Yano K., Goto M., Murakami Morinaga T., Higashio K., Udagawa N., Takahashi N., Suda "Osteoclast differentiation factor is a ligand for osteoprotegerin/osteoclastogenesis-inhibitory factor and to TRANCE/RANKL.";
                                                                                                                                                                                                                                                                                                           Lum L., Wong B.R., Josien R., Becherer J.D., Erdjument-Bromage Schloendorff J., Tempst P., Choi Y., Blobel C.P.;
"Evidence for a role of a tumor necrosis factor-alpha (TNF-alpha) converting enzyme-like protease in shedding of TRAN TNF family member involved in osteoclastogenesis and dendritic
                                                                                                       rto S., Wakabayashi K., Ul
"Crystal structure of the
2.2-A resolution.";
                                                                                                                                                                                        "Crystal structure of the TRANCE/RANKL of receptor-ligand specificity."; J. Clin. Invest. 108:971-979(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ikeda T., Kasai M., Utsuyama M., Hirokawa K.; "Determination of three isoforms of the receptor activator of nuclear factor-kappaB ligand and their differential expression in bone and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21150053; PubMed Ikeda T., Kasai M., Utsu "Determination of three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1; 2
MEDLINE-21150053; PubMed-11250921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and characterization differentiation factor."; Gene 230:121-127(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Osteoprotegerin ligand is a cytokine differentiation and activation."; Cell 93:165-176(1998).
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                                                                                                                                                                                                                                                                                                   survival
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                                                                                                                                                     PubMed=11733492;
                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                                                                    Lam J., Nelson C.A.,
                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                   PubMed=10224132;
                                                                                                                                                                                                                                                                                                                                                                                                                          Endocrinology 142:1419-1426(2001).
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siol. Chem. 277:6631-6630(2002).
FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to FUNCTION: Cytokine that binds to TNFRSF11B/OPG and activation fac TNFRSF11B/ARAK. OSteoclast differentiation and activation fac Augments the ability of dendritic cells to stimulate naive T-proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dendritic-cell function."
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S., Sarosi I., Shalhoub V.,
                                                                                                                                                                                                                                                                                        Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                marrow stroma;
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                                                                                                                                                                                                                                                                                        274:13613-13618(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=10196481;
ra K., Mizuno A.,
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hree isoforms
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                                                                                                                                                                                                                                                                                                                                                                                               PROCESSING,
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                                                                                                                         bukata O., Hayashi S., Okada F., Hata T.;
extracellular domain of mouse RANK ligand
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t G., Scully S., Hsu
C., Eli A., Qian Y.-
G., Guo J., Delaney J
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AB022037;
AB022038;
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AF019048;
AF053713;
AB008426;
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138
197
262
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Gene [6]

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an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy.

SUBUNIT: Homotrimer.

SUBGELLULAR LOCATION: Type II membrane protein and secreted (1soforms 1 and 2); Cytoplasmic (1soform 3).

ALTERNATIVE PRODUCTS: 3 isoforms; 1 (shown here), 2 and 3; iproduced by alternative splicing.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NOTISSUE SPECIFICITY: HIGHLY PRODUCTS AND LYMPH NOTISSUE SPECIFICITY: HIGHLY PRODUCTS AND LYMPH NOTISSUE SPECIFICITY: HIGHLY PRODUCTS AND LYMPH NOTISSUE SPECIFICITY HIGHLY PRODUCTS AND LYMPH NOTISSUE SPECIF

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NOT IN NONLYMPHOID TISSUES AND IS BUT NOT IN B CELLS. A HIGH LEVEL TRABECULAR BONE AND LUNG. AND IS ABUNDANTLY EXPRESSED IN T LEVEL EXPRESSION IS ALSO SEEN IN NODES BUT

by proteolytic processing. The cleavage may be catalyzed by ADAM17. A further shorter soluble form was observed.
DISEASE: DEFICIENCY IN TWESF11 RESULTS IN FAILURE TO FORM LOBULO-ALVEOLAR MAMMARY STRUCTURES DURING PRECHANCY, RESULTING IN DEATH OF NEWBORNS. TRANCE-DEFICIENT MICE SHOW SEVERE OSTEOPETROSIS, WITH ON OSTEOCLASTS, MARROW SPACES, OR TOOTH ERUPTION, AND EXHIBIT PROFOUND GROWTH RETARDATION AT SEVERAL KELETAL SITES, INCLUDING THE LIMBS, SKULL, AND VERTEBRAE AND HAVE MARKED CHONDRODYSPLASIA, WITH THICK, IRREGULAR GROWTH PLATES AND A RELATIVE INCREASE IN HYPERTROPHIC CHONDROCYTES. PTM: N-glycosylated.

PTM: The soluble form of isoform 1 derive the soluble form 1 derive the soluble fo derives from the lyzed by HITH

SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use as long as lo entities requires a or send an email to s requires a license agreement (an email to license@isb-sib.ch) (See http://www.isb-sib. restrictions and EMBL is D for collaboration .ch/announce/ in no way 9

InterPro; IPR003636; TNF_abc. InterPro; IPR000478; TNF_family. Pfam; PF00229; TNF; 1. SMART; SM00207; TNF; 1. PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2; MGI:1100089; Tnfsf11 Differentiation; 13-MAR-02 AAC71061.1; AAB86812.1; AAC40113.1; BAA25425.1; BAA36970.1; BAA36970.1; BAA36970.1; BAA36970.1; BAA36970.1; 3D-structure; BAA97259 99 143 316 139 197 262 117 117 316 48 69 FALSE_NEG W. Receptor; Glycoprotein; Transmembrane; e; Alternative splicing.
TUMOR NECROSIS FACTOR LIGAND SUPERFA JOINED.
JOINED. N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN ISOFORM 3).
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ISOFORM 2). G -> D (IN REF. MISSING (IN REF. CYTOPLASMIC (POTENT: SIGNAL-ANCHOR (TYPE TUMOR NECROSIS FACTOR LIGAND MEMBER 11, SOLUBLE FORM. CLEAVAGE EXTRACELLULAR MEMBER 11, MEMBRANE FORM (POTENTIAL) 08DF63A2BE00967A CRC64; (POTENTIAL) (POTENTIAL). Η MEMBRANE SUPERFAMILY SUPERFAMILY PROTEIN) ŢΡ

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 40, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 5 (CNNSSF5 OR CD40LG OR CD40L.
Canis familiaris (Dog)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                            "Adjuvant properties of canine CD40L.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
                                              ProDom; PD008600; TNE; SMART; SM00207; TNE;
                                                                           InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR00478; TNF_family
Pfam: PF00229; TNF; 1.
                                                                                                                                     EMBL; AF086711; AAD04375.1; HSSP; P29965; 1ALY.
                                                                                                                                                                                or send an
                                                                                                                                                                                                             modified
                                                                                                                                                                                                                                           the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Hosie M.H., Willett B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CANFA
                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277
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                                                                                                                                                                                                                                        European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                proteolytic processing (By similarity).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                          SUBUNIT: HONOTRINER (BY SIMILARITY).
SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
PTM: The soluble form derives from the membrane
                                                                                                                                                                                                                                                                                                                                                                                     proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CANFA
                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKV 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---CQVHFDEGKAV---YLKLDLLV----NGVLALRCLEEFSATAASSPGPQLRL--CQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EESQDVVP-------FLEQLVRPRR--SAPK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMFLALLGLGLGQVVCSIALFLYFRAQMDPNR----ISEDSTHCFYRILRLHENAGLQDST 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLGLALACLGLLLVVVSLGSWATLSAQ-EPSQEELTAEDR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AHYEVHPRPGQDGAQAGVDGTVSGWEE----TKINSSSPLRYDRQIGEFTVIRAGLYYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LESEDTLPDSCRRMKQAFQGAVQKELQHIVGPQRFSGAPAMMEGSWLDVAQRGKPEAQPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67;
PS00251; TNF_1; 1.
PS50049; TNF_2; 1.
; Transmembrane; Glycoprotein; Signal-anchor.
                                                                                                                                                                             requires a license agreement (Son email to license@isb-sib.ch).
                                                                                                                                                                                                          and this statement is not removed.
                                                                                                                                                                                                                           non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                            TNF_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.8%;
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Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 260
                                                                                                                                                                                           (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                     There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .06;
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                                                                                                                                                                                                         Usage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CD40 ligand).
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                                                                                                                                                                                                                                                                    collaboration
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RESULT 6
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Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9ESE2; Q91Z19;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tunor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).
TNFSF11 OR RANKL OR TRANCE OR OPGL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
SITE
DISULFID
CARBOHYD
                                                                                                                                                                              Marks S.C. Jr.;
Marks S.C. Jr.;
"Evidence that the rat osteopetrotic mutation on the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
MCBI_TaxID=10116;
                                                                                                                                               the TNESF11 (TRANCE, RANKL, ODF, OP, Int. J. Dev. Biol. 45:853-859(2001)
-!- FUNCTION: Cytokine that binds to
                                                                                                                                                                                                                                                       Odgren P.R.,
Safadi F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                   PubMed=11804028;
                                                                                                                                                                                                                                                                                                                         STRAIN-Fischer
                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, sequence and homologue of receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zheng M.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20540945; PubMed=11092398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Tibial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu J.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242
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                                                                                                                                                                                                                                                                                                                                                                                       Bone Miner.
             FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to TNFRSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPSQVSHGTGFTSFGLLKL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EASSNPASYLRWAPK-GYYTISSNLVSLENGKQLAVKRQGLYYVYAQVTFCSNRAASSQA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETKINSSSPLRYDRQIGEFT------VIRAGLYYLYCQVHFDEGKAVYLKL
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39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tan J.K.,
                                                                                                                                                                                                                                                                                                                                             OF 266-318
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                                                                                                                                                                                                                                                    Kim N., v. Popoff S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -VASLCLHSPSGTERVLLRAASSRGSSKPCGQQSIHLGGVFELHPGASVFVNVT
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23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bone;
                                                                                                                                                                                                                                                                                                                       344;
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                                                                                                                                                                                                                                                                                                                                                                                       Res. 15:2178-2186(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      and functional characterization tor activator of NF-kB ligand.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huang L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260
112
217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae;
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46
                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                       van Wesenbeeck L.,
S.N., Lengner C., va
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                                                                                                                                                                                                                                                    Lengner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gao X.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 90.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL). CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR LIGAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     604F69A19E98EB70 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318
                                                                                                                                                                                                                                                         van-Hul
                                                                                                                                                                                       gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Laird
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOLUBLE FORM (BY
                                                                                                                                                                                                                                                                          MacKay
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; Murinae; Rat
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RESULT 7

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Matches 64
DOMAIN
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CONFLICT
SEQUENCE
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SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; FALSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF187319; AAG17031.1; -. EMBL; AF425669; AAL23963.1; -. HSSP; P50591; 1D0G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cytokine;
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TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Type II membra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: The soluble form derives from the membrane
                                                                                                                                                                                                                                                                                                               LALLGLGLGQVVCSIALFLYFRAQMDPNR---ISEDSTRCFYRILRLRENTGLQDSTLES
                                                                                                                                                                                                                                                                                                                                          LALACLGLLLVVVSLGSWATLSAQ-EPSQEELTAEDR-----REPPELNPQTEES
                                                                                                                                  GLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQV
                                                                                                                                                                                  QV----HFDEGK--AVYLKLDLLV----NGVLALRCLEEFSATAASSPGPQLRL--CQVS
                                                                                                                                                                                                                                                                                         QD----
                                                                                                        GFFKLRAGEEISVQVSNPSLLDPDQDATYFGAFKV
                                                                                                                                                          NICFRHHETSGSVPADYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVG
                                                                                                                                                                                                            HLTINAADIPSGSH---KVSLSSWYHDRGWAKISNMT----LSNGKLRVNQDGFYYLYA
                                                                                                                                                                                                                                    HYEVHPRPGQDGAQAGVDGTVSGWEE----TKINSSSPLRYDRQIGEFTVIRAGLYYLYC
                                                                                                                                                                                                                                                                EDTEALPDSCRRMKQAFQGAVQRELQHIVGPQRFSGVPAMMEGSWLDVARRGKPEAQPFA
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IPR000478; TNF_family
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(Rel. 14, Created)
(Rel. 29, Last sequence
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199
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317
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                                       STANDARD;
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BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
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                                                                                                                                                                                                                                                                                                                                                                 Score 90.5; DB 1;
Pred. No. 0.72;
6; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
I -> M (IN REF. 2).
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TUMOR NECROSIS FACTOR LIGAND
MEMBER 11, SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE
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MRL outstation -
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EMBL; BC014139; AAH14139.1 EMBL; X07247; CAA30232.1; PIR; A31336; A31336. PIR; A34333; A34333. PIR; S00974; S00974. HSSP; P00634; TAJC. Siena-2DPAGE; P10696; --Genew; HGNC:441; ALPPL2. MIM; 171810; --

EMBL;

ALT_SEQ

EMBL;

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TISSUE-Chorlocarcinoma;
MEDLINE-89308696; PubMed-2745460;
Watanabe T., Li W.L., Soo
"Expression of the germ cell alkaline
chorlocarcinoma cells.";
                                                                                                                                           EMBL;
                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the E
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                             phosphatase-like gene.";
Nucleic Acids Res. 16:5694
-i- CATALYTIC ACTIVITY: An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lowe M.E., Strauss A.W.; "Expression of a Nagao-type, phosphatidylinositol-glycan anchored alkaline phosphatase in human choriocarcinomas."; Cancer Res. 50:3956-3962(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Last annotation update)
Alkaline phosphatase, placental-like precursor (EC 3.:
isozyme) (Germ-cell alkaline phosphatase) (PLAP-like)
                                                                                                                                                                                                                                                                                                                                                                    alcohol + phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-157 FROM N.A.

MEDLINE-88262578; Pubmed-3387245;

Shen L.P., Liu H., Kan Y.W., Kam W.;

"5' nucleotide sequence of a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (SEP-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Millan J.L., Manes T.;
"Seminoma-derived_Nagao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=90283879; PubMed=2162249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPPL2 OR ALPPL
                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                 entities requires a license agreement
                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphatase gene."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: Attached to the membrane by TISSUE SPECIFICITY: TRACE AMOUNTS IN THE TESTIS AND IN ELEVATED AMOUNTS IN GERM CELL TUMORS.
MISCELLANBOUS: IN MOST MAMMALS THERE ARE FOUR DIPLACENTAL, PLACENTAL-LIKE, INTESTINAL AND TISSUE
                                                                                                                                                                                                                                                                           (LIVER/BONE/ KIDNEY).
SIMILARITY: BELONGS TO THE ALKALINE PHOSPHATASE FAMILY.
                                                                                                                J04948; AAA51700.1;
J03252; AAA98616.1;
                                                                                                                                            X55958; CAA39425.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soong B.-W., Chou J.
                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                      human
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i; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                        NON-SPECIFIC
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CONFLICT
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MOD_RES
ACT_SITE
                                          Warzocha
Salles G.
                                                                                                             Browning J.L., Ngam-Ek A., Lawton P., Chow E.P., Hession C., O'Brine-Greco "Lymphotoxin beta, a novel member of heteromeric complex with lymphotoxin Cell 72:847-856(1993).
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CONFLICT
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"Identification of two lymphotoxin beta isoforms expressed lymphoid cell lines and non-Hodgkin's lymphomas."; Biochem. Biophys. Res. Commun. 238:273-276(1997).
                                                                       SEQUENCE FROM N.A. MEDLINE-97445965; E
                                                                                                                                                                                                        TISSUE-T-cell
                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00098; alkPPc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00245; alk_phosphatase; PRINTS; PR00113; ALKPHPHTASE. ProDom; PD001868; Alk_phosphtse
                                                                                                                                                                                       MEDLINE-93208881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001952; Alk_phosphtse
                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGTTDAAHPGPSV----VPALLPLLAGTLLLLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---TAASSPGPQLRLCQVSGLLPLRPGSSLRIRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                      K., Renard
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A
                                                      PubMed=9299492;
rd N., Charlot C.,
                                                                                                                                                                                       PubMed=7916655;
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                                                                                                                                                                                                                    (ISOFORM 1),
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V -> M (II
H -> R (II
L -> R (I
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U -> R (I
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                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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6 (IN REF.
6 (IN REF.
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                                                        Bienvenu
                                                                                                                                                                                                                    PARTIAL
                                                                                                                              , Demarinis J., Tizard R., B., Foley S.F., Ware C.F.; the TNF family that forms on the cell surface.";
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(GLCNAC. . .) (POTENTIAL).
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                                                        Coiffier
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between
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                                                                                     PROSITE;
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EMBL;
PIR; /
                                                                                                              PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF_abc; 1.
SMART; SM00207; TNF; 1.
DOMAIN
                                                      Cytokine; Cy
Alternative
                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                            TRANSMEM
                                          DOMAIN
                                                                                                                                                         InterPro; IPR000478; TNF_family. Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rieder M.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                      InterPro; IPR003636; TNF_abc
                                                                                                                                                                                                        600978;
                                                                                                                                                                                                                                                A46066; A46066.
                                                                                                                                                                                                                    HGNC:6711; LTB
                                                                  PS00251; TNF_1; 1.
PS50049; TNF_2; 1.
Cytotoxin; Transmembrane; Glycoprotein;
                                                      splicing;
 49
                            1
19
                                                                                                                                                                                                                                  1TNR
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POLYMOTPHISM.

B CYTOPLASMIC (POTENTIAL).

8 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

8 (POTENTIAL).

Signal-anchor,

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EMBL; L11016; AAA99888.1; -.
EMBL; U89922; AAC51769.1; -.
EMBL; U79029; AAA37342.1; -.
EMBL; L11015; AAA36191.1; -.
EMBL; Y14768; CAA75069.1; -.
EMBL; AP129756; AAD18089.1; -.
EMBL; AP000505; BAB63395.1; -.
EMBL; AV070219; AAA49954.1; -.
EMBL; AV070219; AAA49955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [3]
SEQUENCE FROM N.A. (ISOFORM 1).
Meville M.J., Milner C.M., Campbell R.D.;
"A new member of the immunoglobulin superfamily and a V-AT
"A new member of the predicted products of novel genes
                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1)
ROWEN L., Madan A., Qin S., Sh
Abbasi N., Dickhoff R., Loretz
Lasky S., Hood L.;
                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (SEP-1997) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific role in immune response regulation. Provides the membrane anchor for the attachment of the heterotrimeric complex to the cell surface. Isoform 2 is probably non-functional.

SUBUNIT: Heterotrimer of either two LTB and one LTA subunits or (less prevalent) one LTB and two LTA subunits.

SUBCELLULAR LOCATION: Type II membrane protein (Potential).

ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.

TISSUE SPECIFICITY: SPLEEN AND THYMUS.

SIMILARITY: BELLONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a S., Tamiya G., Oka A., Inoko H.;
sapiens 2,229,817bp genomic DNA of 6p21.3 HLA clas
tted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (OCT-1999)
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                                                                                                                                                                                                                                                                                                           Usage
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jenes close
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                                                                                                                                                                                                                                                                                                                                                                                     collaboration -
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RESULT
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                                                   WEDLINE-2133568; PubMed-11491535;

Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,

A Weiss W.R., Ansari A.A.;

T "Cloning, sequencing, and homology analysis of nonhuman primate

Fas/Fas-ligand and co-stimulatory molecules.";

L Immunogenetics 53:315-328(2001).

C -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell

proliferation in the absence of co-stimulus as well as IgE

proliferation in the presence of IL-4. Involved in immunoglobuli

C class switching (By similarity).

C -!- SUBURIT: HOMOTRIMER (By similarity).

C -!- SUBURIT: HOMOTRIMER (By similarity).

C --- SUBURIT: HOMOTRIMER (By similarity).

C --- FTM: The soluble form derives from the membrane form by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
VARIANT
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VARSPLIC
           This
                                                                                                                                                                                                 TISSUE-Lymphocytes;
MEDLINE-21383618; P
                                                                                                                                                                                                                                                                                                                                                                               AOTTR
                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member
                                                                                                                                                                                                                                                                                                                       Q9BDM3;
15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                         TNESES OR CD40LG OR CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                               NCBI_TaxID-9505
                                                                                                                                                                                                                                                                             Aotus trivirgatus (Night monkey) (Douroucouli).
                                                                                                                                                                                                                                                                                                                                                                     TNF5_AOTTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SLGLALA---CLGLLLVVVSLGSWATLSAQEPSQEELTAEDR-----REPPEL
                                proteolytic
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                     GLLPLRPGSSLRIRTLPWAHLKAAPFL---TYFGLFQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NPQTEESQDVVPFLEQLVRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVS
           SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                          GLVQLRRGERVYVNI---SHPDMVDFARGKTFFGAVMV 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWEETKINS--SSPLRYDRQIGEFTVIRAGLYYLYCQVHF-----DEGKAVYLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPET----DLSPGLP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SLLLAVAGATSLVTLLLAVPITVLAVLALVPQDQGGLVTETADPGAQAQQGLGFQKLPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLLVNGVLALRCLEEFSATAASSPG-PQLRL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GWETTKEQAFLTSGTQFSDAEG-LALPQDGLYYLYCLVGYRGRAPPGGGDPQGRSVTLRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111
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53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78
70
  Swiss
                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                processing (By similarity).
BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
70
  Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
77
                                                                                                                                                                                                                                                         Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YRAGGAYGPGTPELLLEGAETVTPVLDPARRQGYGPLWYTSVGFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25390
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                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
  ō,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 87;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC...) (POTENTIAL)
GLVTETADPGAQAQOGLGFQKLPEE -> GLGFR.
KQISAPGSQLDTS (IN ISOFORM 2).
MISSING (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB37342).
F41569459830ED4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /FTId-VAR_013026.
DPGAQAQQGL -> GLSAPGSGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /FTId=VAR_013025
                                                                                                                                                                                                                                                        Craniata; Vertebrata; Platyrrhini; Cebidae;
                                                                                                                                                                                                                                                                                                                                                                    PRT;
 Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
           .It is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AAHLIGAPLKGQG-----L
                                                                                                                                                                                                                                                                                                                                                                    261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
1.1;
                                                                                                                                                                                                                                                                                                                                                                    ₹
           produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                              224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; 08
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 and
                                                                                                                                                                                                                                                                                                              (CD40
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                                                                                                              immunoglobulin
the
                                                                                                                                                                                                                                                        Aotinae;
                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IN
                                                                                                                                                                   primate
                                                                                                                                                                                                                                                                                                              ligand) (CD40-
 EMBL
                                                                            exists
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108;
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           a collaboration
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                                                                                                                                                                                                                                                        Aotus
 outstation
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Q
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RESULT 10
TNF5_CALJA
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
SEQUENCE
         Villinger F., Bostik P., Mayne A.E., King C. Welss W.R., Ansari A.A.;
"Cloning, sequencing, and homology analysis Fas/Fas-ligand and co-stimulatory molecules.
Immunogenetics 53:315-328(2001).
                                                                                                                                                                                                                                                                          Q9BDN3;
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2; Cytokine; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                             TISSUE=Lymphocytes;
MEDLINE=21383618; PubMed=11491535;
                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                     Callithrix
                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                             Callithrix jacchus (Common marmoset).
                                                                                                                                                                                                         L) (CD154 protein).
TNFSF5 OR CD40LG OR CD40L.
                                                                                                                                                                                                                                                                                                        TNF5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD002012; TNF_abc; 1. ProDom; PD008600; TNF_5; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P29965;
                                                                                                                                      NCBI_TaxID=9483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     210
                                                                                                                                                                                                                                                                                                                                                                                                                                193
                                                                                                                                                                                                                                                                                                                                                                                                                                                          161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136
                                                                                                                                                                                                                                                                                                                                                                          247 VSHGTGFTSFGLLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 TVSGWEE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVLQWAEKGYYTMSNNLVTLENGKQL---TVKRQGLYYTYAQVTFCSNREASSQAPFIAS
                                                                                                                                                                                                                                                                                                        _CALJA
                                                                                                                                                                                                                                                                                                                                                                                                     LKAAPFLTYFGLFQV
                                                                                                                                                                                                                                                                                                                                                                                                                               --LCLKPPNRFERILLRAANTHSSAKP----CGQQSIHLGGIFELQPGASVFVNVTDPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVLALRCLEEF - - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF344860; AAK37542.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 25.9
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPRQ03263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112
178
240
261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113
Cytokine
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKINSSSPLRYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVN 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
113
218
240
240
29357
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                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     261
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43
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25.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                     224
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -SATAASSPGPQLRLC-----QVSGLLPLRPGSSLRIRTLPWAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Signal-anchor.
TUMOR NECROSIS FACTOR LIGAND
MEMBER 5, MEMBRANE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
 binds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.2;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC. . .) (POTENTIAL); 85E1588B507901B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TUMOR NEĆROSIS FACTOR LIGAND SUPERFAMIL
MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                 Craniata; Vei
Platyrrhini;
                                                                                                                                                                                                                                                                                                        PRT;
 6
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 TNFRSF5.
                                                                                                                                                                                                                                                                                                        261
                                                                                                                                                                  Vertebrata; Euteleostomi;
ni; Callitrichidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                    C.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55;
  Mediates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 261
                                         nonhuman
                                                                                                                                                                                                                                       σ
                                                                    Genain
                                                                                                                                                                                                                                     (CD40 ligand) (CD40-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEMBRANE PROTEIN)
                                         primate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192
                                                                                                                                                                                                                                                                                                                                                                                                                                246
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RESULT 11
TN14_HUMAN
ID TN14_H
AC 043557
DT 16-OCT
DT 16-OCT
DT 15-JUN
DE Tumor 1
DE mediat
GN TNFSF1
OS Homo ss
OC Eukary
OC Mammal
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                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                      TN14_HUMAN STANDARD: PRT; 240 AA. 043557; 075476; Q96LD2; Q8WVF8; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tumor necrosis factor ligand superfamily member mediator-ligand) (HVEM-L).
TNFSF14 OR LIGHT OR HVEML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD002012; TNF_abc; ProDom; PD008600; TNF_5; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPRO03263; TNF_5.
InterPro; IPRO03636; TNF_abc.
InterPro; IPRO03778; TNE_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>:</del>
                Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF344844; AAK37603.1; -.
                                                                                                                                                                                                                                                                      193
                                                                                                                                                                                                                                                                                                  161
                                                                                                                                                                                                                                                                                                                             136
                                                                                                                                                                                                                 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       production in the presence of II-4. Involved in immunogle class switching (By similarity).
SUBUNIT: HOMOTRIMER (By similarity).
SUBCELLULAR LOCATION: Type II membrane protein. Also existancellular soluble form (By similarity).
PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin
                                                                                                                                                                                                                                                                                                                           GVLALRCLEEF -----SATAASSPGPQLRLC----QVSGLLPLRPGSSLRIRTLPWAH
                                                                                                                                                                                                                                        LKAAPFLTYFGLFQV
                                                                                                                                                                                                                                                                    -- LCLKPPNRFERILLRAANTHSSAKP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P29965;
                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                       44
112
178
240
261 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113
 Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
113
218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261
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                                                                                                                                                                                                                                                                                                                                                                                               7.5%;
25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                        29360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal-anchor.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 5, MEMBRANE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                        ₹,
                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                               Score 87;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL) SIGNAL-ANCHOR (TYPE-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLEAVAGE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUMOR NECROSIS FACTOR LIGAND MEMBER 5, SOLUBLE FORM (BY SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                        10CA588D923754EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                   -CGQQSIHLGGIFELQPGASVFVNVTDPSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROSIS FACTOR LIGAND SUPERFAMILY SOLUBLE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 261
                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                    (Herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEMBRANE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outstation
                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                    246
                                                                                                                                                                                                                                                                                                209
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Hac. Genew; ho. 'TM; 604520;

EMBL; EMBL; HSSP; EMBL;

L; AF036581; AAC39563.1; -.
L; AF064090; AAC25169.1; -.
L; AY028261; AAK26160.1; -.
L; BC018058; AAH18058.1; ALT.
P01375; 4TSV.

ALT_FRAME

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as its content http://www.isb-sib.

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collaboration outstation

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HVEM/TR2,
growth.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING. MEDLINE=21528948; PubMed=11673523; Granqer S.W., Butrovich K.D., Houshmand P., Edwards W.R., W. "Genomic characterization of LIGHT reveals linkage to an in response locus on chromosome 19p13.3 and distinct isoforms by alternate splicing or proteolysis."; J. Immunol. 167:5122-5128(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A. (ISUEUM....)
MEDLINE=98122340; PubMed=9462508;
MONTH D.N., Ebner R., Montgomery R.I., Kochel K.D.,
Mirrbhy M., Eisenberg R.J., Cohe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Truneh A., Young P.R.;
"Herpesvirus entry mediator ligand (HVEM-L),
HVEM/TR2, stimulates proliferation of T cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=98438532; PubMed=9765287;
Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J. Tan K.B., Dede K., Spampanato J., Silverman C., Hensley P., DiPrinzio R., Emery_J.G., Deen K., Eichman C., Chabot-Fletcher M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "LIGHT, a new member of the TNF superfamily, ligands for herpesvirus entry mediator."; mmunity 8:21-30(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Homotrimer.
SUBCELLULAR LOCATION: Type II membrane protein and secreted (isoform 1); Cytoplasmic (isoform 2).
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/LIGH: delta-TM; are produced by alternative splicing.
TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BIFOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND TISSUES AND
                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing.

SIMILARITY: BELONGS TO THE TUNOR NECROSIS FACTOR FAMILY.

CAUTION: Ref. 4 sequence differs from that shown due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: N-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NONHEMATOPOIETIC TUMOR LINES.
INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                            frameshift in position 178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND NO EXPRESSION SEEN IN FETAL TISSUES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273:27548-27556(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISOFORM 1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cells and inhibits HT29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENDOCRINE GLANDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a novel ligand for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and lymphotoxin alpha are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cheung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPLEEN BUT ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2/LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune
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Spear P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       generated
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Query Match
Best Local
Matches
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
CARBOHYD
VARSPLIC
                                                   SEQUENCE FROM N.A. (ISOFORM A).

MEDLING-89034212; PubMed-3182834;

Alper S.L., Kopito R.R., Libresco S.M., Lo

"Cloning and characterization of a murine
kidney and from a lymphoid cell line.";

J. Biol. Chem. 263:17092-17099(1988).
                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                         B3A2_MOUSE STANDARD: PRT: 1237 AA.
P13808; Q9ES13; Q9ES12; Q9ES11; Q9ES10; Q9ES09;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2003 (Rel. 41, Last annotation update)
15-JUN-2004 (Rel. 41, Last annotation update)
15-JUN-2005 (Rel. 41, Last annotation update)
15-JUN-2006 (Rel. 41, Last annotation update)
15-JUN-2007 (Rel. 41, Last annotation update)
15-JUN-2008 (Rel. 41, Last annotation update)
15-JUN-2008 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00251; TNF_1; PROSITE; PS50049; TNF_2;
                    SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                               SLC4A2 OR AE2
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                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 SLGLALACLGLLLVVVSLG----SWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVRLRDGTRSYFGAFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRYPEELELLVS-----QOSPCGRATSSSRVWWDSSFLGGVVHLEAGEEVVVRVLDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLKAAP-FLTYFGLFQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLLWETQLGLAFLRGLSYHDGALVVTKAGYYYIYSKVQLGGVGCPLGLASTITHGLYKRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSWEQLIQERRS------HEVNPAAHLTGANSSLTG------
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57; Conserv
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                    ALTERNATIVE
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Pred. No. 1
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L -> V (IN REF. 4).
E -> K (IN REF. 2).
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SIGNAL-ANCHOR (TYPE II MEMBRANE (POTENTIAL).
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CLEAVAGE (POTENTIAL).
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                    SPLICING,
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ne band
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                    TISSUE
                                                                                           H.F.;
3-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GKAVYL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIGAND
                    SPECIFICITY
                                                                                                                                                                                                        Murinae; Mus
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                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Biochem. Biophys. Res.
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EMBL; AF255774; AAG2
PIR; A31789; A31789.
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the European Bioinformatics Institute.
                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00219; ANION_EXCHANGER_1; PROSITE; PS00220; ANION_EXCHANGER_2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lecanda J., Urtasun R.,
"Molecular cloning and
                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                              DOMAIN
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MGD; MGI:109351; S
                                                                                                                                                                      LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTERNATIVE PRODUCTS: 5 isoforms; a (shown here), b1, b2, c1 and c2; are produced by alternative splicing.
TISSUE SPECIFICITY: Isoform a 1s widely expressed at similar levels in all tissues examined. Isoforms b1 and b2 are predominantly expressed in stomach although they are also detected at lower levels in other tissues. Isoform c1 is stomach-specific. Isoform c2 is expressed at slightly higher levels in lung and stomach than in other tissues.

SIMILARITY: BELONGS TO THE ANION EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L; J04036; AAA65505.1; -...

L; AF255774; AAG23154.1; -...

AF255774; AAG23155.1; -...

L; AF255774; AAG23156.1; -...

L; AF255774; AAG23158.1; -...

L; AF255774; AAG23157.1; -...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chem. Biophys. Res. Commun. 276:117-124(2000)
FUNCTION: PLASMA MEMBRANE ANION EXCHANGE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISTRIBUTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lipoprotein;
 AA;
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genomic organization of the
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   Ĭ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transport; Antiport; Ion transport Palmitate; Alternative splicing. CYTOPLASMIC (POTENTIAL).
                    GLREEAVFGAHGCSVCR
A -> G (IN REF. 2)
                                                       MISSING (IN ISOFORM C2).
MISSING (IN ISOFORM C2).
MISSING (IN ISOFORM C1).
ERTSPSPPPTQTPHQEAAPRASKGAQTG
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N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
PALMITATE (BY SIMILARITY)
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   G (IN REF. 2).
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                                      (IN ISOFORM C2)
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) (POTENTIAL).
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Best Local S
Matches 57
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                                                                                                                                                                                                                                  patients
Cell 72:2
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member
L) (TNP-related activation protein) (TRAP) (T ce
                                                                             SEQUENCE FROM N.A.

MEDLINE-93094757; PubMed-1281209;

Spriggs M.K., Armitage R.J., Strockbine L.,

Macduff B.M., Sato T.A., Maliszewski C.R.,

"Recombinant human CD40 ligand stimulates E
immunoglobulin E secretion.";
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with B
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                Aruffo A., Farrington M., Hollenbaugh D., Li X., Milatc Nonoyana S., Bajorath J., Grosmaire L.S., Stenkamp R., Roberts R.L., Noelle R.J., Ledbetter J.A., Francke U., "The CD40 ligand, 9p39, is defective in activated T cel patients with X-linked hyper-IgM syndrome.";
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND VARIANTS MEDLINE-93145330; PubMed-7678782;
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The h
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TNFSF5 OR CD40LG OR CD40L
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SEQUENCE FROM N.A MEDLINE-93138085;
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                                                                                                                                                                                                                                ents with x-linked
72:291-300(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                         human T cell antigen gp39, a member of
nd for the CD40 receptor: expression of
B cell co-stimulatory activity.";
J. 11:4313-4321(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Korthaeuer U., Mages H.W., of TRAP, a ligand for CD40 Immunol. 22:3191-3194(1992).
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                                                             n E secretion.";
176:1543-1550(1992)
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Pred. No. 8.4;
19; Mismatches
                                                                                                     Strockbine L., Clifford K.N., iszewski C.R., Fanslow W.C.; nd stimulates B cell proliferation
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Catarrhini;
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                                                                                                                                                                                                                                                                                                H.D.;
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VARIANTS HIGML FKU-127, ....

MEDILINE-93174270; PubMed=7679801;

Allen R.C., Armitage R.J., Conley M.E., Rosenblatt H.,

Copeland N.G., Bedell M.A., Edelhoff S., Disteche C.M.

Copeland D.K., Fanslow W.C., Belmont J:W., Spriggs M.

Simoneaux D.K., Fanslow W.C., Belmont J:W., Spriggs M.
                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS HIGM1 ARG-36 AND GLY-140.
MEDLINE-93156839; Pubmed-7679206;
KOTThaeuer U., Graf D., Mages H.W., B
Malcolm S., Ugazio A.G., Notarangelo
Kroczek R.A.;
                                               Macchi P., Villa A., Strina D., Sacco M.G., Morali F., B Giliani S., Mantuano E., Fasth A., Andersson B., Zegers Cavaqni G., Reznick I., Levy J., Zan-Bar I., Porat Y., A Plebani A., Vezzoni P., Notarangelo L.D.; "Characterization of nine novel mutations in the CD40 lipatients with X-linked hyper IgM syndrome of various and Am. J. Hum. Genet. 56:898-906(1995).
VARIANTS HIGM1 PRO-155 AND VAL-22
MEDLINE-96133533; PubMed-8550833;
Lin Q., Rohrer J., Allen R.C., La
                                                                                                                                   VARIANTS HIGM1 ALA-126; ARG-140 AND GLU-144.
MEDLINE-95233438; PubMed-7717401;
                                                                                                                                                                                                                                                                                   Nature
                                                                                                                                                                                                                                                                                           MEDLINE-93156840; PubMed-8094231; Disanto J.P., Bonnefoy J.Y., Gaucha de Saint Basile G.; "CD40 ligand mutations in x-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human native soluble CD40L is a bi inside microsomes.";
J. Biol. Chem. 271:5965-5967(1996).
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FEBS Lett. 315:259-266(1993).
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Sci. 7:1124-1135(1998)
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Bonnefoy J.-Y., Gauchat J.-F.;
soluble CD40L is a biologically
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                                          Pfam; PF00229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed entities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
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Hum. Genet. 99:624-627(1997)
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MEDLINE=97295077; PubMed=9150729;
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"Mutations of the CD40 ligand gene
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                                                                                                                                                                                                             J. X68550; CAA48554.1; Z15017; CAA78737.1; L; X67878; CAA48077.1; L; L07414; AAA35662.1; L; D31797; BAA06599.1; J. D31793; BAA06599.1; J. D31795; BAA06599.1; J. D31795; BAA06599.1; J. D31795; BAA06599.1; J. D31796; BAA06599.1; J. D31796; BAA06599.1; J. D31796; BAA06599.1; J. S25684; S25684; S25684; S25684; S25684; S26694; S2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWITCH DEFECT CHARACTERIZED BY ELEVATED CONCENTRATIONS OF SERUM IOM AND DECREASED AMOUNTS OF ALL OTHER ISOTYPES. AFFECTED MALES PRESENT AT AN EARLY AGE (USUALLY MITHIN THE FIRST YEAR OF LIFE) RECURRENT BACTERIAL AND OPPORTUNISTIC INFECTIONS, INCLUDING PAUDIMOCYSTIS CARINII PNEUMONIA AND INTRACTABLE DIARRHEA DUE TO CRYPTOSPORIDIUM INFECTION. DESPITE SUBSTITUTION TREATMENT WITH INTRAVENOUS IMMUNOGLOBULIN, THE OVERALL PROGNOSIS IS RATHER POOM MITH A DEATH RATE OF ABOUT 10% BEFORE ADOLESCENCE.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
NOTE-EUROPEAN CDAOL defect database (mutation db);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: MEDIATES B-CELL PROLIFERATION IN THE ABSE
STIMULUS AS WELL AS IGE PRODUCTION IN THE PRESENCE
INVOLVED IN IMMUNOGLOBULIN CLASS SWITCHING.
SUBUNIT: HOMOTRIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WWW-"http://www.expasy.org/cd401base/";
FTP-"ftp://ftp.expasy.org/databases/cd401base".
DATABASE: NAME-PROW; NOTE-CD guide CD154 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd154.htm".
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SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS EXTRACELLULAR SOLUBLE FORM.
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED ON ACTIVATED CD4+
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DISEASE: DEFECTS IN THESES ARE THE CAUSE OF IMMUNODEFICIENCY WITH HYPER-IGM (HIGM1), AN
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1ALY; 17
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SM00207;
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IPR003636;
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IPR000478; TNF_family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNF5_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                 entities
or send a
                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00251; TNF_1; 1.

PROSITE; PS50049; TNF_2; 1.

Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Disease mutation; Polymorphism; 3D-structure.

CHAIN 1 261 TUMOR NECROSIS FACTOR LIG
                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                     Villinger F., Bostik P., Mayne A.E., King C.L. Weiss W.R., Ansari A.A.; "Cloning, sequencing and homology analysis of
                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=M.mulatta, and C.torquatus atys; MEDLINE=21383618; PubMed=11491535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Macaca mulatta (Rhesus macaque), and Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey). Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily me
                                                                                                                                                                                                                                                                                                                            Fas/Fas-ligand and co-stimulatory molecules.";
Immunogenetics 53:315-328(2001).
-!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                            AND THR-215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNFSF5 OR CD40LG OR CD40L.
             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9BDC7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNF5_MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9544, 9531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 TVSGWEE----TKINSSSPLRYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161
                                                                                                                                                                                                                          proliferation in the absence of co-stimulus as variation in the presence of IL-4. Involved in class switching (By similarity).
SUBGUNIT: Homotrimer (By similarity).
SUBCELULAR LOCATION: Type II membrane protein.
extracellular soluble form (By similarity).
PTM: The soluble form derives from the membrane
                                                                                                                                                                                                 proteolytic
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSHGTGFTSFGLLKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKAAPFLTYFGLFQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVLQWAEKGYYTMSNNLYTLENGKQL---TVKRQGLYYIYAQVTFCSNREASSQAPFIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LCLKSPGRFERILLRAANTHSSAKP---
                          P29965; 1ALY
                                       AF344859;
AF344841;
                                                                                    an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                 non-profit institutions as long and this statement is not removed. requires a license agreement (See an email to license@isb-sib.ch).
           IPR003263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                               processing (By similarity).
BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                      AAK37541.1;
AAK37600.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND
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25.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SATAASSPGPQLRLC-----QVSGLLPLRPGSSLRIRTLPWAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                         M. MULATTA VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        superfamily members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 86; DB Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                               King
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261
                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Lymphocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  member
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                                                                                                                          nere are no restrictions as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLN-60; VAL-204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55;
                                                                                                                                                                                                                                                                                                                                                                        nonhuman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                  Genain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CD40 ligand) (CD40-
                                                                                                                                                                                                                                                                                                              well as
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                                                                                                                                                                                                                              form
                                                                                                                                                                                                                                                                                               vell as IgE
immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                      primate
                                                                                                                                                                                                                                                                                                                                                                                                  C.P.,
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TNF_abc

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RESULT 15
TNF5_MACNE
ID TNF5_MACNE
AC Q9BDM7;
DT 15-JUN-2002
DT TMFSF5 OR CI
OS MACACA neme:
OC Eukaryota;
C Eukaryota;
C CC CETCOPITHEC.
OX NCBL_TaxID=:
RN [1]
CC CETCOPITHEC.
OX NCBL_TaxID=:
RN [1]
RY SEQUENCE FR
RC TISSUE-Lymph
RX Weiss W.R.,
RT TISSUE-Lymph
RX Weiss W.R.,
RT FAS/Fas-1ig,
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Best Local
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CARBOHYD
VARIANT
VARIANT
VARIANT
VARIANT
                                                                                                                TISSUE-Lymphocytes;
MEDLINE-2183618; PubMed-11491535;
Villinger F., Bostik P., Mayne A.E., King C.L.,
                                                                                                                                                                                                                                                                                                                                                                    L) (CD154 protein).
TNFSF5 OR CD40IG OR CD40I.
Macaca nemestrina (Pig-tailed macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD002012; TNF_abc; 1. ProDom; PD008600; TNF_5; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                       "Cloning, sequencing, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9BDM7;
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9545;
                                                                                                                                                                                                                                                                                                                                                             Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105 TVSGWEE----TKINSSSPLRYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVN 160
                                                              proliferation in the absence of co-stimulus of production in the presence of IL-4. Involved class switching (Bv similarit...)
                   class switching (By similarity).
SUBUNIT: Homotrimer (By similarity).
SUBCELLULAR LOCATION: Type II membra
  extracellular soluble form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSHGTGFTSFGLLKL 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKAAPFLTYFGLFQV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --LCLKSPGRFERILLRAANTHSSAKP----CGQQSIHLGGVFELQPGASVFVNVTDPSQ
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206
215
261 AA;
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112
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118
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215
29366 MW;
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178
240
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                                                                                                                                                                                                                                                                                                                                                             Macaca.
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43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein; Signal-anchor; Polymorphism.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21;
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H -> Q (IN M.MULATTA).
I -> V (IN M.MULATTA).
L -> P (IN M.MULATTA).
A -> T (IN M.MULATTA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEMBER 5, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND
MEMBER 5, SOLUBLE FORM (BY SI
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
  II membrane protein.
(By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA2E0F11C0F28ABB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                     TNFRSF5. Mediates |
co-stimulus as well
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                     nonhuman primate
                                                                           as
                                                                                                                                                                                                                                Genain C.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                       Also
                                                                                    immunoglobulin
                                                                                                                        B-cell
                                                                                                       as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
                       exists
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                       as
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Job time: 18.9352 secs
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Best Local S
Matches 34
                                                                                                                                                                                                                                           DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Prodom: PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between the Swiss Institute of Bioinformatics
the European Bioinformatics Institute. There a
use by non-profit institutions as long as i
modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                   SITE
                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF344853; AAK37613.1; -. HSSP; P29965; 1ALY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a
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                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                    TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                            Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD00201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00229;
                                               230
                                                                       214
                                                                                               174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                      PFLTYFGLFQV 224
                                                                                                                                              WAEKGYYTMSNNLVTLENGKQL---TVKRQGLYYIYAQVTFCSNREASSQAPFIAS--LC
                                                                                                                                                             WEE----TKINSSSPLRYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLA 164
                                                                                               LKSPGRFERILLRAANTHSSTKP-----CGQQSIHLGGVFELQPGASVFVNVTDPSQVSHG
                                                                                                                       LRCLEEF - - - - - SATAASSPGPQLRLC - - - - QVSGLLPLRPGSSLRIRTLPWAHLKAA
                                               TGFTSFGLLKL
                                                                                                                                                                                             Similarity 26.(
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Glycoprotein; Signal-anchor.
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23
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                                                                                                                                                                                                       7.3%;
26.0%;
           2003, 07:58:02
                                                                                                                                                                                                                                              MW.
                                                                                                                                                                                             20;
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                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                 MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                CLEAVAGE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                        TUMOR NECROSIS FACTOR LIGAND
                                                                                                                                                                                                                                                                                                                                                                     MEMBER
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                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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alpha-glucosidase,
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ALIGNMENTS

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hypothetical protein PA4851 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa (C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: C83040 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pal A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: C83040 A;Status, oraliminary
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A;Title: Complete Genome Sequence of Caulobacter crescentus. A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: D87394
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C;Accession: D87394
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C;Genetics:
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A; Residues: 1-210 <STO>
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A; Status: preliminary
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Best Local S
Matches 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 LRLGLAVFAAGVAATVIVQAAWRSLASSKLQTQAATAPLVLDKPRF---TGVLKDGRPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 EQLVRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGV----DGTVSGWEETKINSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LSLGLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFL 61
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Similarity 26.2%; Pred. No. 1.6;
33; Conservative 19; Mismatches
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GB:AE004898; strain

GB:AE004091; NID:g9951115; PIDN:AAG08236.1; GSPDB:GN00:

PA01

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A;Residues: 1-421 <STO>
A;Cross-references: GB:AF
A;Experimental source: st
C;Genetics:
A;Gene: PA4851
RESULT 4
$12076
$12076
alkaline phosphatase (EC 3.1.3.1) precursor, placental-like - human
alkaline phosphatase (EC 3.1.3.1) precursor, placental-like - human
N;Alternate names: alkaline phosphatase Nagao isozyme; germ-cell alkaline pl
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 21-Nov-1993 #sequence_revision 13-Mar-1998 #text_change 31-Jan-2000
C;Date: 21-Nov-1993; A34333; S00974; A31336
C;Accession: S12076; I37991; A34333; S00974; A31336
R;Gum, J.R.; Hicks, J.W.; Sáck, T.L.; Kim, Y.S.
Cancer Res. 50, 1085-1091, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Hendra virus
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T08209
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C; Keywords:
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Virology 251, 227-233, 1998
A;Title: The attachment protein of hendra virus has high
A;Reference number: Z16405; MUID:99058172; PMID:9837786
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A; Residues: 1-352 <YUM>
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                                                                                                                                                                                                                                                                                                                                                                                           RPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRAGLY 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVVRSHPEFSGALVVDAITYNRASFSQPFPLLELRFADLNGHLIANRRFKPGEYL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQ 125
                                                                                                                                                                                                                                                        SGLLPLRPGSSLRIRTLPW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IGEFTVI - - - RAGLYYLYCQVHFDE - - - -
                                                                                                                                                                                                                                                                                            YSVEYCKRKIDRMKLQFSLGSIGGLSLHIKINGVISKRLFAQM--
                                                                                                                                                                                                                                                                                                                                 YL--YCQVHFDEGKAVY-----LKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matrix
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trix protein

    Hendra virus

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22.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 89; DB Pred. No. 3.8; 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NID: g3273489; PIDN: AAC83191.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eaton, B.T.; Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
3.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
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                                                                                                germ-cell alkaline phosphatase
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C;Keywords: blocked carboxyl end; glycoprotein; homodimer; lipoprotein; membrane F;1-19/Domain: signal sequence #status predicted <SIG> F;20-503/Product: alkaline phosphatase, placental-like #status predicted <MAT> F;504-532/Domain: carboxyl-terminal propeptide #status predicted <CTP> F;111/Active site: Ser (phosphoserine intermediate) #status predicted F;141.268/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-157 <SHE>
A; Cross-references: EMBL: X07247; NID: g35509
A; Cross-references: EMBL: X07247; NID: g35509
A; Note: the authors translated the codon CCR; Millan, J.L.; Manes, T.
Proc. Natl. Acad. Sci. U.S.A. 85, 3024-3028
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A; Residues: 1-379, 'L', 381-497, 'R', 499-532 .
A; Cross-references: GB:J04948; NID:9178418
R; Shen, L.P.; Liu, H.; Kan, Y.W.; Kam, W.
Nucleic Acids Res. 16, 5694, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:x55558; NID:g296797; PIDN:CAA39425.1; R;Watanabe, S.; Watanabe, T.; Li, W.B.; Soong, B.W.; Chou, J.Y. Biol. Chem. 264, 12611-12619, 1989
A;Title: Expression of the germ cell alkaline phosphatase gene A;Reference number: A34333; MUID:89308696; PMID:2745460
A;Accession: A34333
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A;Residues: 1-177,'A',179-272,'M',274-497,'S',499-530,'T',532
A;Cross-references: EMBL:X53279; NID:928624; PIDN:CAA37374.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      F;185/Binding site: substrate phosphate (Arg) *status predicted F;339,379,451/Binding site: zinc (His) *status predicted F;503/Modified site: GPI-anchor ethanolamine amidated carboxyl ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Seminoma-derived Nagao isozyme is encoded by a A;Reference number: A31336; MUID:88203632; PMID:2834730 A;Accession: A31336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: 5' nucleotide sequence of a putative human placental alkaline phosphatase-li A;Reference number: S00974; MUID:88262578; PMID:3387245 A;Accession: S00974
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A;Residues: 1-56,'M',58-151,'V',153-315,'L',317-532 <MIL>
A;Cross-references: GB:J03252; NID:g178427; PIDN:AAA98616.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: alkaline phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: catalyzes the hydrolysis of phosphate monoesters
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 23/1; 62/1; 100/3; 159/1; 216/3; 261/3; 286/1; 331/1;
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A;Residues: 1-151,'V',153-532 <LOW>
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Best Local S
Matches 44
499
                                                                                                         456
                                                                                                                                                                                                                      400 KARDRKA----YTYLLYGNGPGYYLKDGARPDYTESESGSPEYRQQSAVPLDGETHAGED 455
                                                                                                                                                                                                                                                                         76
                                                   ---TAASSPGPQLRLCQVSGLLPLRPGSSLRIRT 204
                                                                                                                                                                  TVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGV-----
                                                                                                                                                                                                                                                                      KARPRRAIAAHYEV---HPRPG----QDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEF 129
  AGTTDAAHPGPSV----VPALLPLLAGTLLLLGT
                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                         FARGPQAH-----LVHGVQEQTFIAHVMAFAACLEPYTACDLAPP
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28.6%;
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Pred. No: 7.3;
16; Mismatches
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                                                                                                                                                                  -LALRCLEEFSA-----
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PID:g28625
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lymphotoxin beta - human
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Date: 21-Sep-1993  #sequence_revision 18-Nov-1994  #text_change 21-Jul-2000
C:Accession: A46066
R:Browning, J.L.; Ngam-ek, A.; Lawton, P.; DeMarinis, J.; Tizard, R.; Chow, E.P.; |
Cell 72, 847-856, 1993
A:Title: Lymphotoxin beta, a novel member of the TNF family that forms a heteromer.
A;Reference number: A46066; MUID:93208881; PMID:7916655
A;Scatus: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-244 CBRO>
A;Cross-references: GB:L11015; NID:g292276; PIDN:AAA36191.1; PID:g292277
A;Note: sequence extracted from NCBI backbone (NCBIN:128066, NCBIP:128067)
C;Reywords: transmembrane protein
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus. A; Reference number: A87249; MUID:21173698; PMID:11259647
A; Accession: A87348
A; Status: preliminary
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A;Residues: 1-670 <STO>
A;Cross-refrences: GB:AE005673; NID:gl3422039; PIDN:AAK22781.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC0796
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                                                                                                                                                                                 NPQTEESQDVVPFLEQLVRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVS 107
DLLVNGVLALRCLEEFSATAASSPG-PQLRL----
                                             GWETTKEQAFLTSGTQFSDAEG-LALPQDGLYYLYCLVGYRGRAPPGGGDPQGRSVTLRS
                                                                                       GWEETKINS--SSPLRYDRQIGEFTVIRAGLYYLYCQVHF------DEGKAVYLKL 155
                                                                                                                                       EPET----DLSPGLP-
                                                                                                                                                                                                                               SLLLAVAGATSLVTLLLAVPITVLAVLALVPQDQGGLVTETADPGAQAQQGLGFQKLPEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLLPLRPGSSLRIRTLP
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                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                              Score 87;
Pred. No.
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Pred. No. 10;
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3.7;
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Kolon
, C.M.
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band 3-related protein - mouse (; Species: Mus musculus (house mouse) C; Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 2 C; Accession: A31789 R; Libresco, S.M.; Lodish, H.F. R; Alper, S.L.; Kopito, R.R.; Libresco, S.M.; Lodish, H.F. J. Biol. Chem. 263, 17092-17099, 1988 A; Fitle: Cloning and characterization of a murine band 3-related A; Reference number: A31789; MUID:89034212; PMID:3182834
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A;Reference number: A82950;
A;Accession: A83035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, : Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable transmembrane sensor PA4895 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Decies: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 15-Jun-2001 C;Accession: A83035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
A83035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:AE004902; GB:AE004091; NID:g9951162; PIDN:AAG08280.1; A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-340 <STO>
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                                                                                                                                                                                                                                                                                   RVSGTFPVDDLP---LALAMLAQTHGLRLVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLALACLGLLLV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLLPLRPGSSLRIRTLPWAHLKAAPFL - - - TYFGLFQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SL---
                                                                                                                                                                                                                                                                                                                           RPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
                                                                                                                                                                                                                                                                                                                                                                        G-----PVESASEAALAWRQGLLVADDMPLR---QWAGELMRYGGESIE-CEPS-LDPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGAETVLAV-YEGAVQVRP--EGAASAADGRV-----IEAGQRVRFDRQ------RI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARPRRAIAAHYE--VHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRA 134
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67; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas putida regulatory protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of Pseudomonas aeruginosa PAO1, 50; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAEDRREPPELNPQTEESQDVVPFL----EQLVRPRRSAPKGRK 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.4%; Score 86.5;
24.7%; Pred. No. 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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A.; Larbig, K.; L
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A;Molecule type: mRNA A;Residues: 1-1237 <ALP> A;Cross-references: GB:J04036; NID:g192132; PIDN:AAA65505.1; C;Superfamily: band 3 anion transport protein

PID: 9309114

cDNA from kidney

transmembrane

protein

7.48;

Score 86.5;

В

2

Length 1237;

A; Accession: A31789

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A; ACCESSION A
A; Molecule type: mRNA
A; Residues: 1-261 <GAU>
A; Cross references: EMBL: L07414;
A; Cross references: EMBL: L07414;
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A; Residues: 1-261 <SPR>
A; Residues: 1-261 <SPR>
A; Cross-references: GB:X67878; NID:g38411; PIDN:CAA48077.1; PID:g38412
A; Experimental source: peripheral blood T-cell
A; Experimental source: peripheral blood T-cell
A; Graf, D.; Korthaeuer, U.; Mages, H.W.; Senger, G.; Kroczek, R.A.
Eur. J. Immunol. 22, 319-3194, 1992
B:Title: Cloning of TRAP, a ligand for CD40 on human T cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z15017; NID:g38483; PIDN: R;Spriggs, M.K.; Armitage, R.J.; Strockbine, L.; C J. Exp. Med. 176, 1543-1550, 1992
A;Title: Recombinant human CD40 ligand stimulates A;Reference number: JH0793; MUID:93094757; PMID:12 A;Accession: JH0793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Apr-2001
C;Accession: S28017; JH0793; S26694; S28852; I53476; S25684; S30593
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                                                            C;Keywords: glycoprotein; transmembrane protein
F;13-44/Domain: transmembrane #status predicted <TMM>
F;45-261/Domain: extracellular #status predicted <EXT:
F:6,240/Binding site: carbohydrate (Asn) (covalent) #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, EMBO J. 11, 4313-4321, 1992
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                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X68550; NID:g37269; PIDN:CAA48554.1; PID:g37270 R;Gauchat, J.F.; Aubry, J.P.; Mazzel, G.; Life, P.; Jomotte, T.; Elson, GFEBS Lett. 315, 259-266, 1993 A;Title: Human CD40-ligand: molecular cloning, cellular distribution and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: The human T cell antigen gp39, a member of the A; Reference number: S28017; MUID:93049181; PMID:1385114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP
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                                                                                                                                                      A; Map position: Xq26-Xq26
                                                                                                                                                                          A;Gene: GDB:CD40LG; HIGM1; IMD3
A;Cross-references: GDB:120632; OMIM:308230
                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S28852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-261 <GRA>
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57; Conserv
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Similarity
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  . 9 %
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                                                                                                                                                                                                                                                                NID: g180123; PIDN: AAA35662.1; PID: g180124
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9; Mismatches
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  No.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PMID:1280226
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PMID:1281209
  DB
4.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:CAA78737.1; PID:g38484
L.; Clifford, K.N.; Macduff,
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                    Length 261;
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                                                                                                                                                                                                                                             Fig. 2 in
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Am. J. Physiol. 263, usau c. Am. J. Physiol. 261 and lo A; Title: cDNA cloning and lo A; Title: contact and local contac
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C;Accession: A56764
R;Chow, A.; Dobbins, J.W.; Aronson, F
R;Chow, A.; Dobbins, J.W.; Aronson, F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-1237 <CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A; Accession: A56764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               дЬ
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   289 AKGSAQSSREGREPGPTPR 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                          GATPTIEEGEEDEEEANEAEGARAPTEPSPASTPS-SVQFFLQEDEGAERKAERTSPSPP 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVLQWAEKGYYTMSNNLVTLENGKQL---TVKRQGLYYIYAQVTFCSNREASSQAPFIAS 192
                                                                 FSATAASS-----PGPQLR 184
                                                                                                                                                                                                                 RYDRQIGEFTVIRAGLYYLYCQVHFDEGKAVYL---KLDLL------VNGVLALRCLEE 170
                                                                                                                                                                                                                                                                                                  --TLLPHQEAAPW-ATEGAQTGVPVEEVAVVASGTAGGDNGGASGRPLTKAQPGHRSYNL
                                                                                                                                                                                                                                                                                                                                                                        RRATAAHYEVHPRPGQDGAQAGV----
                                                                                                                                           QERRRIGSMTGAEQA---LLPRVPTDESEAQTLATADLDLMKSHRFEDVPGVRRHLVRKN 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224
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Pred. No.
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0; Mismatches
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R;Suda, T.; Takahashi, T.; Gc
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning an
A;Reference number: A49266; M
A;Accession: A49266
                                                                                                                                                                                                                                                                                                  RESULT
A49266
                                                                                                                                                                                                                      C; Date: 13-Jan-1995
C; Accession: A49266
                                    A;Cross-references:
C;Keywords: glycopro
                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SU
                                                                                                                                                                                                                                                             fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
                                    glycoprotein;
                                                                         <SUD>
                                                        GB:U03470; NID:g440178; PIDN:AAC52129.1;
                                                                                                                                                                                                                                          #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
                                      transmembrane
                                                                                                                                                 and expression of the Fas ligand, muID:94084792; PMID:7505205
                                                                                                                                                                                                         Golstein,
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A; Cross-references: EMBL: Z78417;
A; Experimental source: clone C350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C35C5.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: 219173
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                                                                                                                                                                                                                                                                                                                                               A; Map position:
                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP: C35C5.1
                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: Z78543; PIDN: CAB01756.1; GSPDB: GN00028; CESP: C35C5
                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                  RPRRAIAAHYEVHPRPGQDGAQAGV--DGTVSGWEETKI-----NSSSPLRYDRQIGEF 129
                                                                                                                                                                                                                                   QEPSQEELTAEDRREPPELNPQTEESQDVV-----PFLEQLVRPRRSAPK-----GRKA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYKL
                                               GLLPLRPGSSLRIR
                                                                            GRVKESTLSKTIEQYLQAGKLVSPKCD
                                                                                                         TVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVS 189
                                                                                                                                                                                                    EQELEEHLRNAYRHEEEEC --- FEEEDDIIELPPLPVKPAVKKPRRKLPKHLSIESGSTA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLFQV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YCTTGQI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGLYYLYCQVHFDEGKA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TK-KPRS--VAHLTGNPRSRSIPLE-----WEDTYGTALISGVKYKK--GGLVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINS-SSPLRYDRQIGEFTVIR 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVGMGLGMYQLFHLQ-----KELAELREFTNHSLRVSSFEKQIANP--STPSE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKG
                                                                                                                                        KTSKLVAEVVHDHPRPVNYRMKPAVTDDGKVVEQKRTRVTRNIMSHTIPQYHLEGEETEF
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                                                                                                                                                                                                                                                                    l Similarity
42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             1-2962 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278
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                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                               7.2%; Score 84; DB 2;
21.6%; Pred. No. 1.1e+07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.9%;
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                                                                                                                                                                                                                                                                  29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIDN:CAB01693.1; GSPDB:GN00028; CESP:C35C5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 7.8;
0; Mismatches
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                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                               1.1e+02;
                                                                            -QFREQIVATAVEYDG-SVKMLQFE
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                                                                                                                                                                                                                                                                                                Length 2962;
                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                                                                                1587,
                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-467 <SEE>
A;Cross-references: EMBL:AL109849; PIDN:CAB52866.1; GSPDB:GN00070;
A;Experimental source: strain A3(2)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
A; Gene: SMb21182
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H95947
                                                                                                                                                                                   hypothetical protein SC3A3.09 - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #tex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-394 <KUR>
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SCOEDB:SC3A3.09
                                                                                                                                                                                                                                                                                                                               LRIRTLPWAHLKAAPFLTY 218
                                                                                                                                                                                                                                                                                                                                                             AQRERTGEGQQIDMALLDCMTGVLANQALNFL--
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63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                 AHPNIAPYQVE
                                                                                                                                     D.; James, K.D.; Parkhill,
ata Library, August 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.3%;
                                                                                                                                                                                                                                                                                                 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 83.5;
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Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Geession: H95947
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A;Experimental source: Strain 1021, megaplasmid pSymB
R;Gallbert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors; Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weldner, S.; Wells, D.H.; Wong, K.; Yeh,
A;Title: The composite genome of the legume symbiont Sinorhizobium mediiloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable conserved membrane-anchored protein SMb21182 [imported] - Sinorhizobium
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C;Accession: H95947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Genome: plasmid C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv3272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LLLVVVSLGSW-----ATLSAQEPSQEELTAEDRRE--PPELNPQTEESQDVVPFLEQLV 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLLPLRPGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGFGQDGPYAHRAGYDYIVQGMSGIMDLTGEPDREPQKIGVAFADIFTGLYGVIAVQAAL
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                                                                                                                                                                                                                                   J.; Barrell,
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                                                                                                                                                                                                                                   B.G.; Rajandream,
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SCOEDB: SC3A3
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A:Molecule type: mRNA
A:Residues: 1-24, 'L',26-65,'V',67-262,'H',264-276,'R',278-284,'A',286-388,'C',A:Cross-references: GB:M14170; NID:g178469; PIDN:AAA51709.1; PID:g178470
A:Note: parts of this sequence, including the amino end of the mature protein A:Note: this is polymorphism type 3; 89-Leu also found
R:Millan, J.L.
The control of the mature protein A:Molecular polymorphism type 3; 89-Leu also found
                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 23-535 <HRN>
A; Cross-references: GB:M14169
A; Note: parts of this sequence, including the amino end
A; Note: this is polymorphism type 1; 67-Leu also found
A; Accession: B24318
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross references: GB:M19160
R;Henthorn, P.S.; Knoll, B.J.; Raducha, M.; Rothblum, K.N.; Proc. Natl. Acad. Sci. U.S.A. 83, 5597-5601, 1986
A;Title: Products of two common alleles at the locus for hum A;Reference number: A94113; MUID:86287303; PMID:3461452
A;Accession: A24318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-535 KNO
A; Cross references: GB: J03931;
A; Knoll, B.J.; Rothblum, K.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alkaline phosphatase (EC 3.1.3.1) precursor, placental [validated] - human N;Alternate names: glycerophosphatase; orthophosphoric-monoester phosphohydrolase, C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 30-Sep-1987 #sequence_revision 28-Jul-1995 #text_change 08-Dec-2000 C;Date: 30-Sep-1987 #sequence_revision 28-Jul-1995 #text_change 08-Dec-2000 C;Accession: A31074; A27363; A24318; B24318; A25385; A94099; A94082; A28958; A90114 R;Knoll, B.J.; Rottblum, K.N.; Longley, M. J. Biol. Chem. 263, 12020-12027, 1988
                                                                         J. Biol. Chem. 261, 3112-3115, A;TItle: Molecular cloning and A;Reference number: A25385; MU A;Accession: A25385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Nucleotide sequence of the human placental alkaline A;Reference number: A31074; MUID:88298886; PMID:3042787 A;Accession: A31074
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A;Title: Two gene duplication
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A; Residues: 1-76 <KN2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A27363
                                                  Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAENIDGMPEDDDLNYPLLGLLLLRRHGKAFTTGDVARVWLDELPPGRTFTAERVALRNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ELNPQTEESQDVVPFLEQLV--RPRRSAPKGRKAR-----PRRAIAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTGLEPPHTARHRNPFREWIGALIRADVHGW----TNPGDP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----HYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRAGLYY
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57; Conserv
                               1-230,'P'
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      P',232-535 < GB:M13077;
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23.6%;
                                                                                             and sequence analysis of human; MUID:86140079; PMID:3512548
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<MIL>; NID:g178471;
                                                                                                                                         1986
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Longley, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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         PIDN: AAC97139
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      PID:g178474
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Search Job tim

completed: March ne : 33.5442 secs

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A;Description: catalyzes the hydrolysis of phosphate monoesters C;Superfamily: alkaline phosphatase C;Keywords: blocked carboxyl end; glycoprotein; homodimer; lipoprotein; F;1-22/Domain: signal sequence #status predicted <SIG>F;23-506/Product: alkaline phosphatase, placental #status experimental < F;507-535/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;114/Active site: Ser (phosphoserine intermediate) #status predicted F;144.271/Binding site: carbohydrate (Asn) (covalent) #status predicted F;342,382,454/Binding site: zinc (His) #status predicted F;342,382,454/Binding site: zinc (His) #status predicted F;506/Modified site: GPI-anchor ethanolamine amidated carboxvl end (Asn)
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A; Residues: 382-435, 'T', 437-535 < OVI>
A; Residues: 382-435, 'T', 437-535 < OVI>
A; Residues: 382-435, 'T', 437-535 < OVI>
A; Note: a soluble or serum form was also found that may ari A; Note: a soluble or serum form was also found that may ari A; Nam, W., Clauser, E.; Klm, Y.S.; Kan, Y.W.; Rutter, W.J.
Proc. Natl. Acad. Sci. U.S.A. 82, 8715-8719, 1985
A; Title: Cloning, sequencing, and chromosomal localization A; Reference number: A94082; MUID:86094295; PMID:3001717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 485-535 (MIC)
A; Residues: 485-535 (MIC)
R; Ezra, E.; Blacher, R.; Udenfriend, S.
Biochem. Biophys. Res. Commun. 116, 1076-1083, 1983
Biochem. Biophys. Res. Commun. 116, 1076-1083, 1983
A; Title: Purification and partial sequencing of human
A; Reference number: A90114; MUID:84079906; PMID:665184
A; Accession: A90114
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A;Title: Expression of different-sized placental alkaline A;Reference number: A94099; MUID:86233318; PMID:3459156
A;Accession: A94099
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A;Map position: 2q37.1-2q37.1
A;Introns: 26/1; 65/1; 103/3; 162/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 23-64 <EZR> C; Comment: This is the fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A28958; A; Accession: A28958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 6-24,'L',26-260,'GE',263-323,'H',325-395,'FI',398-400,'A',402-535 <KAM>A;Cross-references: GB:M12551; NID:g178463; PIDN:AAA51706.1; PID:g178464
R;Micanovic, R; Bailey, C.A.; Bs, K.; Geber, L.; Pan, Y.C.E.; Hulmes, J.D.; Ude Proc. Natl. Acad. Sci. U.S.A. 85, 1398-1402, 1988
A;Title: Aspartic acid-484 of nascent placental alkaline phosphatase condenses with A;Reference number: A28958; MUID:88144444; PMID:3422741
g
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A; Residues: 6-24, 'L',
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                                                                                                                                                                                                                                                                  76 KARPRRAIAAHYEV---HPRPG---QDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEF 129
                                                                                                                                                                                                                                                                                                                          Local Similarity
les 43; Conserv
                                                    ---TAASSPGPQLRLCQVSGLLPLRPGSSLRIRT
                                                                                                                                                                                                                   KARDRKA----YTVLLYGNGPGYVLKDGARPDVTESESGSPEYRQQSAVPLDEETHAGED
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27.98;
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PMID:6651840
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Command line parameters:

MODEL-frame+p2n.model DEV-xlh

-WODEL-frame+p2n.model DEV-xlh

-Q-/ggn2_1/USPTQ_Spool_VS9245198/runat_24032003_163552_25944/app_query.fasta_1.846

-DB-N_Geneseq_101002 -QFMT-fastap -SUFFIX-rng -MINMAYCH=0.11 -LOOPCL=0

-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX-bitsum62 -TRANS-human40.cdi

-LIST-45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15

-MODE-LOCAL -QUTFMT-pto -NORM=ext -HEARSIZE-500 -MINLEN=0 -MAXLEN=20000000

-MODE-LOCAL -QUTFMT-pto -NORM=ext -HEARSIZE-500 -MINLEN=0 -MAXLEN=200000000

-USER-US09245198_@CGN_1_1_338_@runat_24032003_163552_25944 -NCPU=6 -ICPU=3

-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WALIT -LONGLOG -DEV_TIMEOUT=120

-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7

-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - nucleic search, using frame_plus_p2n model
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SUMMARIES

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ALIGNMENTS

AAV18599
ID AAV18599 standard; cDNA; 1168 BP.

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AC AAV18599;
XX
DT 21-JUL-1998 (first entry)
XX
DE Mus musculus tumour necrosis factor related ligand (TRELL) gene.
XX
KW TRELL; tumour necrosis factor related ligand; tnf; treatment;
XX
KW cancer; autoimmune disease; immune system; stimulation; suppression;
XX
VX
OS Mus musculus.
XX
FH Key
CDS
Location/Qualifiers

Location/Qualifiers

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Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that encoding mouse tumour necrosis factor related ligand (TRELL). TRELL or active fragments can be included with a carrier in pharmaceutical compositions to treat cancer, autoimmune diseases or immune responses to tissue grafts, or to stimulate or suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for, can then be administered, optionally with interferon- gamma, to induce cell death or treat, suppress or alter immune responses (especially involving human adenocarcinoma cells) involving a signal pathway between TRELL and its receptor. The DNA sequence can be used in gene therapy for TRELL-related disorders in mammals (especially humans), e.g. tumours, autoimmune and inflammatory diseases or inherited genetic disorders, by introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL. It may also be of use in the preparation of prepare probes for screening natural/synthetic DNAs for TRELL-encoding sequences
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18-OCT-1996;
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                                                              P-PSDB; AAW93591.
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New Tumor Necrosis Factor family receptor polypeptides useful for diagnosis and treatment of prostate cancer $\boldsymbol{\varepsilon}$

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC This invention describes isolated Tumor Necrosis Factor (TNF) family CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer by determining levels of APO4 is useful for diagnosing prostate cancer completely. APO4 polypeptides are also useful for identifying selective binding agents linked to a therapeutic completely. APO4 polypeptides are also useful for identifying selective binding of contety. APO4 polypeptide/active fragment which is extracellular, or completely agents to the polypeptide/active fragment which is extracellular, or completely active fragment which is extracellular, or completely active fragments are also useful for screening completely active fragments are also useful for screening composites by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or completely active fragments are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact continue and APO4 signal transducer molecules that specifically interact continue and APO4 signal transducer molecules that specifically interact continue and APO4 signal transducer molecules that specifically interact continue and APO4 signal transducer molecules that specifically interact continue and APO4 signal transducer molecules that specifically interact continue and APO4 signal transducer molecules that specifically interact continue and APO4 signal transducer molecules that specifically interact continue and APO4 signal transducer molecules that specifically interact continue and APO4 and detecting a change in level of APO4 and detecting a change in level of APO4 and detecting a change in level of APO4 and apost transferted to human heaset carcinum call line about the about the apost attended to human heaset carcinum call line and apost attended to human heaset carcinue.
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                 AlaAlaSerSerProGlyProGlnLeuArgLeuCysGlnValSerGlyLeuLeuProLeu
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                                                                                                                                                                                                                The TNF-related endothelium proliferative agent (TREPA), or its activators or agonists, are used to treat a deficit of TREPA, e.g. to promote wound healing or tissue grafting, by promoting vascularisation, also to induce apoptosis for treating cancer and eliminating autoreactive T cells, as an adjunct to cancer chemotherapy or antiviral treatment. TREPA peptides can also be used to target cytotoxic agents or for affinity isolation of the corresponding receptor, the nucleic acid for which can be used to transform tumour cells to render them more responsive to TREPA and to screen for TREPA mimics.
                                                    conditions involving abnormal stimulation of epithelial cells atherosclerosis), for birth control (inhibiting ovulation and formation) or other angiogenic conditions (e.g. ulcers).
                                                                                                                                   Ribozymes, antisense RNA, antibodies or peptides, are used to treat TREPA-associated diseases, e.g. tumours and metastases (by inhibiting vascularisation), inflammation or a wide range of autoimmune conditions,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting nucleic acid encoding TREPA - useful for diagnosis and treatment of autoimmune disease, tumours and inflammation
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P-PSDB; AAW29745.
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                                                                                                                                           TNF; angiogenesis; wound healing;
proliferative agent; tumour; metastasis;
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                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molecules designated as TREPA (TNF related endothelium proliferative agent). Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis in human for promoting wound healing and for vascularising grafted tissue for successful grafting and to promote tissue grafts. The present sequence is a cDNA clone ID #690050 encoding human TREPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inducing angiogenesis in mammal at desired sites for promoting wound healing, by administering soluble fragment of extracellular domain of tumor necrosis factor related endothelium proliferative agent protein
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DB; AAE00891.
                                                                                    AACCGACTAGTTCGGCCTCGAAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGA
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Novel composition to inhibit neoplastic cell growth or for treating tumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO2021, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or
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Query Match:
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(ANTCC 209358) encoding human pRO207 (see ANY95338), which shows to monology to several members of the tumour necrosis factor family, especially human lymphotoxin (23.4%). The cDNA was identified in a foetal kidney cDNA library following identification of an expressed sequence tag with homology to human Apo-2 ligand. A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell to pRO179, pRO207, PRO320, PRO219, PRO221, PRO224, PRO3101, PRO526, PRO320, PRO3209 or PRO866 (see ANY95337-49), their agonists or chimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, contral nervous system cancer, melanoma and leukaemia. Nucleic acids encoding PRO179 etc. are used in the recombinant production
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253 61 312

313 62

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373 82

102 ValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSerSerProLeuArg

433 GTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGC

122 TACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACCTGTACTGT TyrAspArgGlnIleGlyGluPheThrValIleArgAlaGlyLeuTyrTyrLeuTyrCys

142 493 GlnValHisPheAspGluGlyLysAlaValTyrLeuLysLeuAspLeuLeuValAsnGly

161

141 492 121

612

CAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGT

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IleArgThrLeuProTrpAlaHisLeuLysAlaAlaProPheLeuThrTyrPheGlyLeu

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26-JUL-1999
28-JUL-1999
31-AUG-1999
01-SEP-1999
polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignat tumours (e.g. renal, kidney, bladder, breast, etc), leukaemlas and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO polypeptides of the invention.
                                                                                                                                      Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
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inflammatory disorder; immune disorder; angiogenic disorder;
gene therapy; cytostatic; neuroprotective; gene; ss.
                                                                                               The present invention relates to the isolation of novel human
                                                                                                                     Claim
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99US-133459P.
99WO-US12252.
99US-140650P.
99US-140653P.
99US-146598P.
99US-146598P.
99US-146522P.
99US-14598P.
99US-14598P.
99US-14598P.
99US-151689P.
99US-US20111.
99WO-US2011.
99WO-US2011.
99WO-US20313.
99WO-US20313.
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Pan J, P
Wood WI;
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Query Match:
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Query
                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to 592 polynucleotides which have been derived from CC a variety of human tissue sources and which encode novel secreted CC proteins. The polynucleotides can be used as probes for the CC identification and isolation of full length cDNA and genomic DNA. The polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies and disorders such as viral infections, bacterial infections, fungal infections, autoimmune disorders (e.g. rheumatoid arthritis, multiple cs clerosis, autoimmune thyroiditis and diabetes) and allergic reactions and conditions (e.g. asthma). They are also useful for treating neurodegenerative diseases (e.g. Alzheimer's disease, parkinson's CC and conditions (e.g. coagulation disorders (e.g. haemophilla), CC inflammatory disorders (e.g. Crohn's disease) and tumours. They are also useful for treating to burns, incisions and ulcers. The proteins are also useful for regulating the burns, incisions and for treating myeloid or lymphoid cell deficiencies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour; autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer; coagulation disorder; inflammatory disorder; Crohn's disease; incision; tissue regeneration; wound healing; burn; haematopoiesis; myeloid cell deficiency; lymphoid cell deficiency.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Five hundred and ninety two polynucleotides derived from a va-
human tissue sources which encode secreted proteins, useful for
treating immune deficiencies and disorders such as autoimmune
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07-AUG-1996;
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WPI; 1998-145619/13
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GlnValHisPheAspGluGlyLysAlaValTyrLeuLysLeuAspLeuLeuValAsnGly
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BIOGEN INC.
UNIV GENEVA FACULTY MEDICINE
                                                                                                                                                                                                                                                                                                                                                                 tumour necrosis factor related ligand
                                                                                                                                                                                                                                                                                                                                   necrosis factor related ligand; tnf; treatment;
                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                     immune system;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119and (TRELL). TRELL or active fragments can be included with a carrier in pharmaceutical compositions to treat cancer, autoimmune diseases or immune responses to tissue grafts, or to stimulate or suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for, can then be administered, optionally with interferon-gamma, to induce cell death or treat, suppress or alter immune responses (especially involving human adenocarcinoma cells) involving a signal pathway between TRELL and its receptor. The DNA sequence can be used in gene therapy for TRELL-related disorders in mammals (especially humans), e.g., tumours, autoimmune and inflammatory diseases or inherited genetic disorders, by introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL. It may also be of use in the preparation of prepare probes for screening natural/synthetic DNAs for TRELL-encoding sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour necrosis factor related ligand - useful for, e.g. treating cancer, auto-immune disease and immune responses to tissue grafts {\sf cancer},
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1373 BP;
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ValLeuAlaLeuArgCysLeuGluGluPheSerAlaThrAlaAlaSerSerProGlyPro
                                         TyrAspArgGlnIleGlyGluPheThrValIleArgAlaGlyLeuTyrTyrLeuTyrCys
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||CacaaccgccagatcgggagttTaTaGTCACCCGGGCTGGGCTCTACTACCTGTACTGT
                                                                                                                                                                                                                  GTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGC
                                                                                                                                                                       ValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSerSerProLeuArg
                                                                                                                                                                                                                                                                          AACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGAAAACACGGGCTCGAAGA
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                                                                                                                                                                                                                                                                                                                                              AGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGCTGGTGGCAGAGGAGGAC
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RESULT 9
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                                                                                Percent Similarity:
Best Local Similari
                                                                                                                               Score:
                                                                                                                                                                     Alignment
                                                                                                                                                                                                                                                                                The present sequence encodes a human tumour necrosis factor (TNF) are lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has cytostatic activity. Apo-3 ligand can be used to induce apoptosis in mammalian cancer cells, to induce NF-kappaB-dependent transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX56000;
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                         to induce JNK/SAPK-dependent responses in
                                                                                                                                                                                                                                                                                                                                                                                           Claim 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ashkenazi AJ,
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10-OCT-1997;
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NF-kappaB-dependent transcription; JNK/SAPK-dependent res
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                                                                                  Similarity:
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RESULT 10
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CF Expre
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                                                                                                                          corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic join preneoplastic condition; myocardia angiogenesis; wound granulation; scleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atherosclerosis; peripheral atherosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAKR;
                                                                                                                                                                                                                                                                                  ocular neovascularisation; diabetic retinopathy; neovascular glaucoma; retinoblastoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; ds;
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                                                                                                                                                                                                                                                                                                                                                                        TWEAK extracellular domain; tumour necrosis factor; TNF; angiogenesis;
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the isolation of human TWEAK receptor (TWEAKR)-expressing clones

of from a COS cell human cDNA library. The TWEAK protein is a

member of the tumour necrosis factor (TWF) family and induces

angiogenesis. TWEAKR may therefore be used to screen for and develop

TWEAKR agonists and antagonists for the modulation of angiogenesis, to be

used in the treatment and diagnosis of human disease. The disorders

mediated by angiogenesis include ocular disorders characterised by ocular

neovascularisation such as diabetic retinopathy, neovascular glaucoma,

retinoblastoma, retinopathy of prematurity, retrolental fibroplasia,

rubeosis, uveitis, macular degeneration and corneal graft

neovascularisation, and inflammatory diseases such as arthritis,

rheumatism and psoriasis. Other treatable diseases include malignant and

metastatic conditions such as sarcomas and carcinomas, benign tumours and

preneoplastic conditions, myocardial angiogenesis, haemophilic joints,
                                                        scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telangiectasia, wound granulation, tatherosclerosis, peripheral atherosclerosis and ischaem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents a DNA from the expression vector pDC409-LZ-TWEAK, which encodes a fusion protein comprising a grownorne leader, a leucine zipper multimerisation domain, and the extracellular domain of human TWEAK. The fusion protein was used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 39-40; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac peripheral tissue, by administering antagonist or agonist of TWEAK
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Scores:

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                                                                 Chaudhary PM,
                                                                                                                                                               05-SEP-1997;
                                                                                                                                                                                                             04-SEP-1998;
                                                                                                                                                                                                                                                             11-MAR-1999
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New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
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Example VII; Fig 13A; 156pp; English.

This invention describes isolated Tumor Necrosis Factor (TNF) family CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active concern their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic CC moiety. APO4 polypeptides are also useful for identifying selective CC binding agents, useful in diagnosis/treatment of disease by binding of CC agents to the polypeptide/active fragment which is extracellular, or CC expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/active fragments are also useful for screening CC for agonists and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vivo or in vitro. APO polypeptides are all useful as immunogens for preparing antibodies. APO4 is also CC useful for diagnosis/treatment of developmental or gestational CC abnormalities. APO8 was transfected to human breast carcinoma cell line MCF-7, and induced apoptosis.

Sequence 1030 BP; 223 A, 317 Ç 279 ç; 211 Τ; 0 other;

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US-09-245-198A-2
                Query Match:
DB:
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Best Local Similarity:
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                                                                Alignment Scores:
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                      Length:
Matches:
Conservative:
Mismatches:
Indels:
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(1-225) x AAX23424 (1-1030)

480		Db 4
177	158 LeuValAsnGlyValLeuAlaLeuArgCysLeuGluGluPheSerAlaThrAlaAlaSer :	Qy
420	361 TACCTGTACTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTG	Db 3
157		Qy
360		Db 3
137	118 SerProLeuArgTyrAspArgGlnIleGlyGluPheThrValIleArgAlaGlyLeuTyr	0у 1
300	٠.	Db .
117	98 AlaGlnAlaGlyValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSer	Qy
240		Db 1
97	78 ArgProArgArgAlaIleAlaAlaHisTyrGluValHisProArgProGlyGlnAspGly (Qy
180	121 GCGCCTTTCCTGAACCGACTAGTTCGGCCTCGCAGAAGTGCCACCTAAAGGCCGGAAAACA 180	Db 1
77	58 ValProPheLeuGlnLeuValArgProArgArgSerAlaProLysGlyArgLysAla :	Qy
120	61 GCAGAGGAGGACCAGGACCCGTCGGAACTGAATCCCCAGACAGA	DЬ
57	38 AlaGluAspArgArgGluProProGluLeuAsnProGlnThrGluGluSerGlnAspVal	Qy
60	1 GTCAGTTTGGGGAGCCGGGCATCGCTGTCCGCCCAGGAGCCTGCCCAGGAGGAGCAGCTGGTG	₽
37	18 ValSerLeuGlySerTrpAlaThrLeuSerAlaGlnGluProSerGlnGluLeuThr 37	Qy

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                              New Drosophila tumour necrosis factor molecule, useful in agriculturally important pests, e.g. comprises modifying feeding or reproduction of crop-damaging insects or insec
                                                                  WPI; 2002-195121/25.
P-PSDB; AAU77718.
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                                                                                                                                                                                                                                                                                                                                 sig_peptide
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                                                                                           Carroll PM,
                                                                                                                                                                     21-MAR-2000; 2000US-190816P
                                                                                                                                                                                     20-MAR-2001; 2001US-0813329
                                                                                                                                                                                                      31-JAN-2002
                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                            Tumour necrosis factor; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding tumour necrosis factor variant 2 (TNFv2).
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                                                                                                                                    (RAMA/)
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GUAN B.
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/*tag= b
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                                                                                                                                                                                                                                                                                      /product= "TNFv1"
/note= "Tumour necrosis
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                      note= "Specifically claimed"
                                                                                                                                                                                                                                                /*tag=
                                                                                                                                                                                                                                                               /label= mature_TNFv1
                                                                                                                                                                                                                                                                        /*tag=
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GCGGGAGGGAAACAACCGAAGCTACTTTGGCATCTTCAAGGTG
                                                 uLysAlaAlaProPheLeuThrTyrPheGlyLeuPheGlnVal
                                                                                                  CCTGGAACGAAACGAGGATCCATCTGAAGGACATTCACAACGATCGCAATGCAGTTCT
                                                                                                                                                oLeuArgProGlySerSerLeuArgIleArgThrLeu----
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ABK11679 standard; DNA; 1221

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Thus the polypeptide and polynucleotide may be useful for treating, ameliorating or preventing %-linked anhidrotic (hypohidrotic) ectodermal dysplasia and X-linked anhidrotic (hypohidrotic) ectodermal dysplasia-like disorders, e.g. sparse hair, abnormal or missing teeth or sweat gland aberrations in animals (e.g. insects and potentially humans), endotoxic shock, inflammation, haemorrhagic necrosis of tumours, cytotoxicity and obesity-linked insulin resistance, all of which involve TNF molecules. This sequence encodes the drosophila melanogaster tumour necrosis factor variant 1(TNFvI) protein, described in the invention.
                                                                                                                                                                                                                                            (TNF). The polypeptide and polynucleotide are useful in controlling agriculturally important pests, particularly by modifying the growth, feeding and/or reproduction of crop-damaging insects or insects of farm animals. The polypeptide and polynucleotide are useful for modulating epithelial morphogenesis, cell-matrix adhesion in files and mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Drosophila tumour necrosis factor molecule, useful in controlling agriculturally important pests, e.g. comprises modifying the growth, feeding or reproduction of crop-damaging insects or insects of farm animals
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(XIAO/)
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          27-SEP-2001
                                                    Drosophila melanogaster
                                                                          pharmaceutical;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enhancement for the accordance to the second content of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 978 BP;
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11-JUL-2000;
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  ACGGTGCCCACCAACATGCCACATAAGGTGCACACCTGCCACACGAGTGGTCT
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                                                                    This cDNA encodes a murine RANKL, a ligand for the RANK (receptor care activator of necrosis factor-kappab (NF-RB)) polypeptide. RANK is a member of the tumour necrosis factor (TNF) family. A soluble RANK comember of the tumour necrosis factor (TNF) family. A soluble RANK contacting a cell expressing membrane-associated RANK with a soluble RANK which binds to CR RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be used to induce maturation of dendritic cells and enhance their colls and enhance their colls and enhance their colls and enhance their colluble RANK polypeptide composition may also be used for regulating an immune or inflammatory response. Inhibition of NF-kB by RANK antagonists compose that result from triggering of RANK, e.g. in treating toxic response that result from triggering of RANK, e.g. in treating toxic contactons. They can also be used in adjunct therapy for disease characterised by neoplastic cells that express RANK. RANKL polypeptides can also be used in flammatory of the colls of the colls.
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23-DEC-1996;
07-MAR-1997;
                          an inflammatory response, and also for protecting RANK-expressing cells from the negative effects of chemotherapy or the presence of high levels of TNF-alpha. The products can also be used for detection and drug
                                                                                                                                                                                                                                                                                                                                                      Claim
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                                                                                                                                 SerGlyLeuLeuProLeuArgProGlySerSerLeuArgIleArgThrLeuProTrpAla 208
                                                                                                                                                                 GGAGGGAGCACGAAAAACTGGTCGGGCAATTCTGAATTCCACTTTTATTCCATAAATGTT
                                                                                                                                                                                          PheSerAlaThrAlaAlaSerSerProGlyProGlnLeuArgLeu-----CysGlnVal 188
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Command line parameters:

-MODEL-frame+_p21.model -DEV-xlh
-Q-/cgn2_1/USPTO_Spool_VS9045198/runat_24032003_163553_25950/app_query.fasta_1.846
-Q-/cgn2_1/USPTO_Spool_VS9045198/runat_24032003_163553_25950/app_query.fasta_1.846
-DB-GEDEMb1 -QFMT-fastap -SUFFIX=rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09245198_0CGN_1_1_3077_@runat_24032003_163553_25950 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NUSCORES=0 -WAXLT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
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30: em_htg_hum:*
31: em_htg_other:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_mus:*
35: em_htg_rod:*
36: em_htg_mam:*
36: em_htg_mam:*
37: em_htg_other:*
40: em_htgo_hum:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae
1 (bases 1 to 1168)
Chicheportiche, Y., Bourdon, P.R., Xu, H., Hsu, Y.M., S.
Hession, C., Garcia, I. and Browning, J.L.
TWEAK, a new secreted ligand in the tumor necrosis
that weakly induces apoptosis
J. Biol. Chem. 272 (51), 32401-32410 (1997)
98070015
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Chicheportiche, Y., Bixler, S.,
Direct Submission
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AF030100.1 GI:2707220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-OCT-1997) Cell Cambridge, MA 02142, USA
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//db_xref="GI:2707221"
//translation="VLSGALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREP
/*translation="VLSGALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREP
PELNOQTEESQDVVPFLEQLVRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGV
DGTVSGWEETKINSSSFLRYDRQIGEFTVIRAGLYYLKCQVHFDEGKAVYLKLDLLVN
GVLALRCLEEFSATAASSPGPQLRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
/cell_type="peritoneal macrophages"
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                                                            LeuSerLeuGlyLeuAlaLeuAlaCysLeuGlyLeuLeuValValValValSerLeuGly
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AACCGACTAGTTCGGCCTCGAAGAAGTGCACCTAAAGGCCGGAAAAACACGGGGCTCGAAGA
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Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 1306)
Chicheportiche,Y., Bourdon,P.R., Xu,H., Hsu,Y.M., So
                                                                                                                                                      Bourdon,P., Hession,C., Tizard,R. and Direct Submission Submitted (14-OCT-1997) Cell Biology, Cambridge, MA 02142, USA
                                                                                                                                                                                                                    Hession, C., Garcia, I. and Browning, J.L.
TWEAK, a new secreted ligand in the tumor necrosis
that weakly induces apoptosis
J. Biol. Chem. 272 (51), 32401-32410 (1997)
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/protein_id="AAC51923.1"
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                                                         /note="ligand in the TNF family; secreted
codon not verified experimentally"
                                                                            /tissue_type="tonsil"
18. .767
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                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                            Location/Qualifiers
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US-09-245-198A-2 (1-225) x AF030099 Percent Similarity: Best Local Similarity: PheGlnValHis ValLeuAlaLeuArgCysLeuGluGluPheSerAlaThrAlaAlaSerSerProGlyPro GlnValHisPheAspGluGlyLysAlaValTyrLeuLysLeuAspLeuLeuValAsnGly TACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACCTGTACTGT TyrAspArgGlnIleGlyGluPheThrValIleArgAlaGlyLeuTyrTyrLeuTyrCys GTGCTGGCCCTGCGCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCCCTCGGGCCC CAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGT GTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGC ValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSerSerProLeuArg CAGGACCCGTCGGAACTGAATCCCCAGACAGAAGAAAGCCAGGATCCTGCGCCTTTCCTG AX201324 Sequence 3 AX201324 AX201324.1 247 Ð RPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH"
434 c 368 g 257 t ARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGL YYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLAL from 764 9.95e-69 1020.00 92.86% 88.84% 87.78% 9 GI:15391154 Patent W00153486 368 g (1-1306)Length:
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Mismatches:
Indels: ďď DNA 1306 199 9 16 0 linear PAT 181 161 141 452 121 101 692 632 572 512 392 332 81 61 212 41 752 221 201 272 152

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TTCCAGGTTCAC
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Ashkenazi,A.J., Goddard,A., Godowski,P.J., Gurney,A.L.,
Hillan,K.J., Marsters,S.A., Pan,J., Pitti,R.M., Roy,M.A.,
Stone,D.M., Watanabe,C.K. and Wood,W.I.
Compositions and methods for the treatment of tumour
Patent: WO 0153486-A 3 26-JUL-2001;
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Mammalia; E
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             SerTrpAlaThrLeuSerAlaGlnGluProSerGlnGluGluLeuThrAlaGluAspArg
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Homo sapiens Apo3/DR3 ligand
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Marsters,S.A., Sheridan,J.P., Pitti,R.M., Brush,J., Goddard,A. and
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South San Francisco, CA
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YYLYCQVHFDEGKAYYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLAL
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58. .807
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1 (bases 1 to 898)
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266 c 267 g 178 t
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52. .873
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                                                                                                                                                                                            /note="human TWEAK fusion
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                                 Direct Submission

Direct Submission

Submitted (07-DEC-2001) National Institutes of Health, Mammalian Submitted (07-DEC-2001), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
           NIH-MGC Project URL: http://mgc.
Contact: MGC help desk
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1651)
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Series: IRAL Plate: 30 Row: p Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4507596.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 30 Row: p Column: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: nisc_mgc@nhgri.nih.gov
ShevChenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
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Web site: http://www.nisc.nih.gov/
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superfamily, member 12"
/protein_id="AAH190471"
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ARRAIAAHYEVHPRPGQDGAQADGGYTTCLRP"
a 517 c 481 g 309 t
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/db_xref="taxon:9606"
/clone="MGC:20669 IMAGE:4766071"
/tissue_type="Primary B-Cells from Tonsils"
/clone_lib="NIH_MGC_48"
/lab_host="DH10B-R"
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Matches:
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Mismatches:
Indels:
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http://image.llnl.gov
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REFERENCE AUTHORS TITLE JOURNAL	RESULT 8 AC069459/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	Qy Db 1	Оу :	Db Oy	Qу	Qy	Qy Db	Qу	Оy	Db	Qy	Вb	Qy	Db 4
ORS ORS	ULT 8 05459/c US INITION ESSION SION WORDS RCE RCE RGANISM	222	202	182 (960 (162 ' 900 (142 (122 : 780 :	102 1	101	600 (100 -	540 (100	80
<pre>lia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musases 1 to 203083) asses 1 to 203083) cr, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C., ich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., On, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z., C., Bunac, C., Delgado, O., Ding, Y., Dugan-Rocha, S., ndez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., ndez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., ll, J., H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M., Hou, X., Huber, J., Jackson, L., Jozado, R.J., Martin, R., Y., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R., Y.E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S., Y.E., McLeod, M.P., Mei, G., Moren, N., Oguh, M., Parish, B., L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S., amson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A., J. M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G., y.K. and Gibbs, R.</pre>	459 203083 bp DNA linear HTG 27-JUN usculus chromosome 11 clone RP23-168P5, WORKING DRAFT NCE, 7 unordered pieces. 459 459 23 GI:14547768 HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP. usculus. usculus. usculus. usculus usculus.	PheGlnValHis 225 TTCCAGGTTCAC 1091	IleArgThrLeuProTrpAlaHisLeuLysAlaAlaProPheLeuThrTyrPheGlyLeu 221 	GlnLeuArgLeuCysGlnValSerGlyLeuLeuProLeuArgProGlySerSerLeuArg 201 	ValLeuAlaLeuArgCysLeuGluGluPheSerAlaThrAlaAlaSerSerProGlyPro 181 	GlnValHisPheAspGluGlyLysAlaValTyrLeuLysLeuAspLeuLeuValAsnGly 161 	TyrAspArgGlnIleGlyGluPheThrValIleArgAlaGlyLeuTyrTyrLeuTyrCys 141 :::	ValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSerSerProLeuArg 121 	AGAAGAGAGACACATCTCCCCACCATTACCAGAGGGTCAAAGGAGAACAAGAGACAAGAGT 719	CAGGGGTGAGGGGTCCATGCAGGGGCCACATCCAAAAAGGGGGAGGGA	100	CCCAGCTAGAATGTGCCTGTGTACTGGACATGGTCTGCATGAAAGGCGAGGTGGCTGGTG 599	100	TGGAGGTTACACAACTTGTCTGAGGCCATGAGATACTAAGTGGTGGAGCCAAGATTTGAA 539

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Best Local Similarity:
                                                                                                                                                                                                                                                 Score:
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43305 TCAGGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCCT 43246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                      100 AlaGlyValAspGlyThrValSerGlyTrpGluGluThrLysIleAsnSerSerSerPro 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemistry: Dye-primer Bodipy: 48% of reads (Chemistry: Dye-terminator Big Dye: 52% of reads Assembly program: Phrap; version 0.990329 (Consensus quality: 212648 bases at least Q40 (Consensus quality: 218902 bases at least Q30 (Consensus quality: 218902 bases at least Q30 (Consensus quality: 222384 bases at least Q20 (Consensus quality: 222384 bases at least Q20 (Consensus quality: 222384 bases at least Q20 (Consensus quality: 210556; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 7.2x in Q20 bases; sum-of-contigs estimation
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Center clone name: RP23-168P5
----- Summary Statistics
Sequencing vector: M13; L0882:
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62253
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118873
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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/db_xref="taxon:10090"
/chromosome="11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62152: contig of 62152 bp in length 62252: gap of unknown length 118772: contig of 56520 bp in length 118872: gap of unknown length
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                                                                                                                                                                                                                                                                  Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 20, 2001 this sequence version replaced gi:16605765.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
                                                                                               complete sequence. AL603707
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-422L16 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                     database can be found at
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                                                                                   TREMBL; Wp:, WORMPEP; Information on the WORMPEP
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om clone RP23-422L16
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unordered pieces.
AC016876 5 GI:21313830
HTG: HTGS PHACETI PIECE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 177703)
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/note="Sequence from uni-directional primer reads and big dye terminator reads only."
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Example of Charles Street, Cambridge, MA 02141, USA CE 3 (bases 1 to 17703)

Birren, B., Nusbaum, C., Lander, E., All.A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Comarata, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, JS., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Gardham, L., Grand-Pierre, N., Hagos, B., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacCenthy, M., Weldrim, J., Meneus, L., Mihova, T., Mandthews, C., McCarthy, M., Weldrim, J., Meneus, L., Mihova, T., Menga, V., McCarthy, M., Weldrim, J., Norell, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Sman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Scojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Direct Suhmission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 2, 2002 this sequence version replaced gi:15421989. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                             as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L3849
Center clone name: 186_B_7
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Center: Whitehead Institute/ MIT Center for Genome
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                                                 48646 48745: gap of 100 bp
48746 58277: contig of 932 b
58278 58377: gap of 100 bp
58378 65804: contig of 7427 b
65805 65904: gap of 100 bp
65905 79793: contig of 13889
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79793: contig of 13889 bp in length
79893: gap of 100 bp
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/db_xref="taxon:9606"
/clone="RP11-186B7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-JUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Akhter, N., Antonellis, A., Ayele, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It current consists of 15 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nmalia; Eutheria; Pr
(bases 1 to 215795)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 203929 bases at least 040 Consensus quality: 206865 bases at least 030 Consensus quality: 206865 bases at least 020 Consensus quality: 209181 bases at least 020
                      49443
60957
61057
74521
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30151
30251
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15640
15740
24776
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Insert size: 214395; sum-of-contigs
Quality coverage: 7.30x in Q20 bases; agarose-fp
Quality coverage: 6.47x in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: nisc_zoo@nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: NIH Intramural Sequencing Center Center code: NISC
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3694
8002
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     soy3: gap of unknown leng
8001: contig of 4308 bp 1
8101: gap of unknown leng
15639: contig of 7538 bp in
15739: gap of unknown length
24775: contig of 9036 bp in
24875: gap of unknown length
30150: contig of 5275 bp in 1
0250: gap of unknown length
9212: contig of 8962 bp in 1e.
1312: gap of unknown length
342: contig of 8962 bp in 1e.
142: gap of unknown length
142: gap of unknown length
142: gap of unknown length
156: contig of 10300 bp in len
16: gap of unknown length
16: contig of 11514 bp in len
16: gap of unknown length
16: contig of 13464 bp in len
17: gap of unknown length
18: contig of 13464 bp in len
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of 13464 bp :
unknown lengt
of 14902 bp :
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/db_xref="taxon:9598"
/clone="RP43-145D13"
/clone_lib="RP43"
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54859 c 53752 g 53513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J.,
Haghighi,P., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Lari,
Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
Margulles,E.H., Masiello,C., Maskeri,B., Mastrian,S.D.,
McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R.,
Portnoy,M.E., Prasad,A., Schueler,M.G., Stantripop,S., Thomas
Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.,
Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.,
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (08-AUG-2002) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 177555)
Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sus scrofa
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 177555)
                Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.990319 consensus quality: 164120 bases at least Q40 consensus quality: 168085 bases at least Q30 consensus quality: 170767 bases at least Q20 Insert size: 169000; agarose-fp
                                                                                                                                                                                                                                               Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
                                                                                                                                                                                                       Center clone name: 436K21
                                                                                                                                                                                                                            Center project name: dbg
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Insert size: 176655; sum-of-contigs
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Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-245-198A-2 (1-225) x AC130192 (1-177555)
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/db_xref="taxon:9823"
/clone="RP44-436K21"
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l. .3460
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13465: contig of 6496 bp in length
13565: gap of unknown length
21301: contig of 7736 bp in length
21401: gap of unknown length
21401: gap of unknown length
33719: contig of 12318 bp in length
33819: gap of unknown length
45054: contig of 11235 bp in length
45144: gap of unknown length
45144: gap of unknown length
58724: contig of 13570 bp in length
58824: gap of unknown length
16670: contig of 17846 bp in length
76670: gap of unknown length
115165: contig of 38395 bp in length
115265: gap of unknown length
115265: gap of unknown length
115265: gap of unknown length
117555: contig of 62290 bp in length
117555: contig of 62290 bp in length
177553: contig of 62290 bp in length
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                                                 Conservative: Mismatches: Indels:
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                                  Gaps:
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RES AC1 LOC DEF ACC VER KEY SOU O	Db 04	Qy Db	οğ	Qy Db	Db Qy	Db	ν	DЪ	Qy	рь	Db Qy	Db Qy	Db Qy	Db 04	P 04	Db Qy	Qу
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AC126925 AC126925 AC126925 Vertebrata; Clone RP81-332E11, WORKING DRAFT SEQUENCE, 15 AC126925 AC126925 AC126925 AC126925 AC126925 AC126925 AC126926 AC126927 AC12692	oPheLeuThrTyrPheGlyLeuPheGlnValHis 225 	uArgProGlySerSerLeuArgIleArgThrLeuProTrpAlaHisLeuLysAlaAlaPr 214 	rAlaAlaSerSerProGlyProGlnLeuArgLeuCysGlnValSerGlyLeuLeuProLe 194 	SLEUASPLEULEUVALASNGlyValLEUAlaLEUArgCySLEUGlUGlUPHESERALATH 174 		GCTGGGAAGGATGCCGGGCCTCTTGGGAAACCTGAGACAGGGTCAAGGGCAAGCAGAGGC 114254	141	AAGGGTTGCTGGGGGGGGGGGGGGGGCCCCAAGTTAAAAGTGGGGAAGGGGGAGGTTTGT 114314		TyrTyrLeuTyrCys141	SerSerProLeuArgTyrAspArgGlnIleGlyGluPheThrValIleArgAlaGlyLeu 136	GlyAlaGlnAlaGlyValAspGlyThrValSerGlyTrpGluGluThrLySIleAsnSer 116 ::: ::	AlaArgProArgArgAlaIleAlaAlaHisTyrGluValHisProArgProGlyGlnAsp 96	ValValProPheLeuGluGlnLeuValArgProArgArgSerAlaProLysGlyArgLys 76	ThralaGluAspArgAluProProGluLeuAsnProGlnThrGluGluSerGlnAsp 56	SerTrpAlaThrLeuSerAlaGlnGluProSerGlnGluGluLeu 36	LeuAlaCysLeuGlyLeuLeuValVal

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TITLE
JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-JUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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Consensus quality: 148712 bases at least Q40
Consensus quality: 151471 bases at least Q20
Consensus quality: 153125 bases at least Q20
Insert size: 152000; agarose-fp
Insert size: 16028; sum-of-contigs
Quality coverage: 5.36x in Q20 bases; agarose-fp
Quality coverage: 5.10x in Q20 bases; sum-of-contigs
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Best Local Similarity:
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                          42566 GTGGGGAGCCTAGGGTCGGGGCCCGATGGGATCCTGGGGTCACCAAGGACCCCGGACTCT 42507
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                                                                                                                                                                                                                                                             GGAAGCGGGGCCCCAGGTTGAGGGAGACGGAGAGGGTTTGGTTCAGGGGGCAGGTTGGG 42567
                                                                                                                                     CGGGCTGGGCTCTACTACCTGTACTGCCAGGTAAGCCCCACCTGGCTCCACGGTAGGGCA 42627
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68780. .78984
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31902. .40781
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27950. .31801
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41863 c 41233 g 37340
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131786. .161428
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                                                                                                                                                                                                    Barbaria, J. Benton, J. Binage, K., Blankenburg, K., Bonnin, D., Bunck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bunck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bunck, J., Chavez, D., Carton, T. F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., Davis, C., Davy-Carroll, L., Dederich, D.A., Davis, C., Davy-Carroll, L., Dederich, M. H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garza, N., Gill, R., Goutell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Garlis, T., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlyson, E., Kally, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Lu, X., Lucier, A., Martindale, A., Martinez, E., Mahshari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Mossey, M., Rojus, M., Ren, Y., Peters, L., Pickens, R., Paims, E., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Payton, B., Peery, J., Royse, A., Rojas, A., Rojubokan, L., Rolfe, M., Ruiz, S., Savery, G., Sobter, G., Shen, H., Shooshtari, N., Sisson, I., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H.,
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                          Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Wilcon, C., Wu, Y., E., Zhou, J., Zorrilla, S., Nelson, D., Wolfer, S., Shou, J., Zorrilla, S., Nelson, D., Wolfer, S., 
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AC119115.2 GI:21746718
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         Weinstock, G. and Gibbs, R.
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23, *** SEQUENCING
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Baylor Plaza, Houston,
On Jul 14, 2002 this se
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (25-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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Direct Submission
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Unpublished
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NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   as soon as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jul 14, 2002 this sequence version replaced gi:20303440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 138792)
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Chemistry: Dye-terminator Big Dye: 100% of re
Assembly program: Phrap; version 0.990329
Assembly program: Phrap; version 1 least Q40
Consensus quality: 116766 bases at least Q30
Consensus quality: 119165 bases at least Q20
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Direct Submission
Submitted (10-JUL-2002) NIH Intramural Sequencing
Submitted (10-JUL-2002) NIH Intramural Sequencing
Grovemont Circle, Gaithersburg, MD 20877, USA
Grovemont Circle, Gaithe
                                                                                                                                                                          * runs of N, but the exact sizes of the gaps are unknown * This record will be updated with the finished sequence
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Bos taurus clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
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                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: ddi
Center clone name: 045D24

Center clone name: 045D24

Center clone name: 045D24

Center clone name: 045D4

Sequencing vector: plasmid; n/a; 100% of reads chemistry: Dye-terminator Big Dye; 100% of reads chemistry: 146066 bases at least Q30 consensus quality: 147748 bases at least Q30 consensus quality: 147748 bases at least Q30 consensus quality: 148024 bases at least Q20 Insert size: 151000; agarose-fp contigs quality coverage: 8.80x in Q20 bases; sum-of-contigs quality coverage: 8.72x in Q20 bases; sum-of-contigs
                                                                                as soon as it is available be preserved.
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Contact: nisc_zoo@nhgri.nih.gov
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2312: contig of 2312 bp in 2412: gap of unknown length
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Percent Similarity:
Best Local Similarity:
Query Match:
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25224: contig of 9325 bp in length
25324: gap of unknown length
32504: gap of unknown length
32504: gap of unknown length
40070: contig of 8366 bp in length
41070: gap of unknown length
56590: contig of 15520 bp in length
56690: gap of unknown length
13869: gap of unknown length
90859: contig of 16990 bp in length
111428: gap of unknown length
111528: gap of unknown length
1553: contig of 20469 bp in length
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AlaHisLeuLysAlaAlaProPheLeuThrTyrPheGlyLeuPheGlnValHis
                                                                           GlyLysAlaValTyrLeuLysLeuAspLeuLeuValAsnGlyValLeuAlaLeuArgCys 167
                                                                                                                                                                                              GAGCGTGGGGTTTGGGCTGAGAGGAGCCTTGGGCCTCTAAGGACACCTGAGATGAAGCCC 27146
                                                                                                                                                                                                                                     CCGGAACTGAAGGAGAAAGGCTGGGCTTCGGGGTTTGGGGGCCAAGTTAAAGGTGGGGAAGGG 27086
                                                                                                                                                                                                                                                                          CGGGCTGGGCTGTACTACCTGTACTGTCAGGT-AAGCCCCCACCTGGCTCCACGGGTAAAG 27026
                                    GGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGACACGCTGGCCCTGCGCTGC
                                                                                                                                                       ------HisPheAspGlu 147
 27440
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Search completed: March 31, Job time: 3276.48 secs 2003, 04:35:32 THIS PAGE BLANK (USPTO)

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Perfect score:
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length DB	ength	DB	ID	Description
1	1162	100.0	225	19	AAW47524	Mus musculus tumou
N	1162	100.0	225	21	AAB07527	Amino acid sequenc
ω	1089	93.7	211	20	AAW93591	Mouse TNRL3 protei
4	1020	87.8	249	19	AAW29745	TNF related endoth
5	1020	87.8	249	20	AAY09369	Human tumour necro
6	1020	87.8	249	21	AAB07526	Amino acid sequenc
7	1020	87.8	249	21	AAY95338	Human PRO207 antit
8	1020	87.8	249	22	AAE00891	Human TREPA (TNF r
9	1020	87.8	249	23	AAU86129	Human PRO207 polyp
10	1020	87.8	284	19	AAW47525	Homo sapiens tumou

4.4	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
90	90	90.5	90.5	90.5	90.5	91	91	92	96.5	97	99	102.5	102.5	102.5	102.5	102.5	102.5	102.5	102.5	103	106.5	106.5	106.5	106.5	106.5	107.5	110.5	111	721	742	4	951	951
7.7	7.7																												2	ω.		1	
261	182	531	318	260	211	294	182	261	409	255	234	316	316	316	316	316	316	316	316	220	294	294	294	294	294	325	409	406	146	189	189	273	208
18	18	10	22	21	21	18	18	23	23	22	22	23	21	21	21	20	19	19	19	22	22	22	22	19	19	22	23	23	22	22	19	22	20
AAW09115	AAW24011	AAP91776	AAB82092	AAY58215	AAY58216	AAW09123	AAW09128	AAM4 9225	AAU77716	AAB86311	AAB62339	AAU78289	AAY84419	AAY84418	AAY91024	AAY17874 .	AAW59654	AAW83017	AAW83194	AAB62340	AAE01992	AAE04425	AAE08737	AAW68292	AAW69956	ABB67553	AAU77718	AAU77717	AAE00895	AAE00892	AAW29746	AAU03499	AAW93590
Human CD40L mutein		m cell alkal	c	Canine CD154. Can	Canine mature CD15		CD40 ligand/zipper	Human CD145 mutant	Drosophila melanog	_	Gp120 V3 loop-CD15			aci	Mouse OBM protein		Amino acid sequenc	O		Gp120 V3 loop-CD15	RANKL (re	Murine receptor ac			חי			Drosophila melanog	Human TREPA (TNF r		æ	extrac	Human TNRL3 protei

ALIGNMENTS

PA XX	Y P P ;	P X P	X P X	P X	4 H H	FH	XX SO	× z	KW	Κ¥	XX XX	XX X	X A	AAW4 XX	RESU
(BIOJ) BIOGEN INC. (UYGE-) UNIV GENEVA FACULTY MEDICINE.	07-AUG-1996; 96US-0023541. 18-OCT-1996; 96US-0028515.	U/-AUG-1997; 9/WO-US13945. 18-MAR-1997: 97US-0040820.		WO9805783-A1.	Domain 121 /note= "hydrophobic, transmembrane domain"	Key Location/Qualifiers	Mus musculus.	gidit rejection.	ne dise	TRELL; tumour necrosis factor related ligand; tnf; treatment;	Mus musculus tumour necrosis factor related ligand (TRELL).	21-JUL-1998 (first entry)	AAW47524;	AAW47524 ID AAW47524 standard; Protein; 225 AA. XX	RESULT 1

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RESULT 2
AABO7527
ID AABO
XX AABO
AC AABO
XX AABO
XX TWEA
KW TWEA
KW TWEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC ligand (TRELL). TRELL or active fragments can be included with a CC carrier in pharmaceutical compositions to treat cancer, autoimmune CC diseases or immune responses to tissue grafts, or to stimulate or CC suppress the immune system. It is useful to screen for TRELL CC receptors, by labelling with a detectable label and screening CC compositions for binding. Agents interfering with TRELL-receptor CC compositions for binding. Agents interfering with TRELL-receptor CC phinding can also be screened for, can then be administered, optionally with interferon-gamma, to induce cell death or CC continually with interferon-gamma, to induce cell death or CC treat, suppress or alter immune responses (especially involving human CC adenocarcinoma cells) involving a signal pathway between TRELL and its receptor. It's coding sequence can be used in gene therapy for CC TRELL-related disorders in mammals (especially humans), e.g. tumours, CC autoimmune and inflammatory diseases or inherited genetic disorders, by introducing into cells, and expressing, therapeutically effective CC amounts of a vector, e.g. a virus comprising a gene encoding TRELL. CC streening natural/synthetic DNAs for TRELL-encoding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 225
                                                                                                                TWEAK protein; immunological disorder; immune response; inflammation; TWEAK blocking agent; autoimmune disease; organ transplant rejection; Graft-versus-Host disease; GVHD; lymphoid cell malignament.
                   20-JUL-2000
                                                                                                                                                                                         Amino acid
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                                                    WO200042073-A1
                                                                                    Mus sp
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                                                                                                                                                                                                                                                                                           AAB07527 standard;
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                                                                                                                                                                                       sequence
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                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                     entry)
                                                                                                                                                                                     of a soluble recombinant murine TWEAK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1162; DB 19; 100.0%; Pred. No. 1.3e-112;
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Best Local
                                                                                                                            developmental abnormality; gestational abnormalitity; prostate cancer; APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          describes a method for preventing or treating an immunological disorder and/or inhibiting an immune response in an animal. The method comprises administering a TWEAK blocking agent. The method may be used for preventing and treating immune disorders associated with inappropriate expression and/or activity of TWEAK. These disorders include autoimmune diseases, acute and chronic inflammation, organ transplant rejection, Graft-versus-Host disease (GVHD), lymphoid cell malignancies, septic and other forms of shock, loss of immune
                                                                                               apoptosis;
                                                                                                              cytoplasmic
                                                                                                                                                        Tumour necrosis factor receptor; signal transducer
                                                                                                                                                                                     Mouse TNRL3
                                                                                                                                                                                                                                              AAW93591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a TWEAK protein. The specification describes a method for preventing or treating an immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Preventing and treating immune responses using modulators, especially antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, useful for treating e.q. inflammation and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                responsiveness (as seen in human immunodeficiency virus (HIV) infections) and failure of the immune response to tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 45pp; English.
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                                                                                                              domain;
                                                                                                                                                                                     protein.
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                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0116168
                                                                                                              immunogen; antibody
                                                                                                                                                                                                                                                                         211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1162; DB 21;
Pred. No. 1.3e-112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   versus host disease
                                                                                                             preparation; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                           225
                                                                                                                                                          molecule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                              carcinoma;
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11-MAR-1999 W09911791-A2

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RESULT 4
AAW29745
ID AAW2
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AC AAW2
AC AAW2
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AC TOF
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TOF
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TOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC This invention describes isolated Tumor Necrosis Factor (TNF) family CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 is useful for diagnosing prostate cancer CC be treated using APO4 selective binding agents linked to a therapeutic CC moiety. APO4 polypeptides are also useful for identifying selective CC binding agents, useful in diagnosis/treatment of disease by binding of CC agents to the polypeptide/active fragment which is extracellular, or CC expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/active fragments are also useful for screening CC or agonists and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active fragments are broad active that specifically interact CC with a cycoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vivo or in vitro. APO polypeptides also CC are all useful as immunogens for preparing antibodies. APO4 is also cuseful for diagnosis/treatment of developmental or gestational and accordate approach of the change of apochesis of apochesis and accordate to human breast carcinoma cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local 9
                                    TNF related endothelium proliferative agent protein.
                                                                                                                      AAW29745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
                                                                                27-OCT-1998
                                                                                                                                                           AAW29745 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 40; Fig 13B; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX23425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MCF-7, and
                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                               195
                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 LVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Н
                                                                                                                                                                                                                                                                                                                                                    GLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLLPL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                RKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRA 134
endothelium proliferative agent; TREPA; wound healing; cancer;
                                                                                                                                                                                                                                                     RPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVVVSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-205191/17.
                                                                                                                                                                                                                                                                                           RPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
                                                                                                                                                                                                                                                                                                                                  GLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLLAL
                                                                                                                                                                                                                                                                                                                                                                                                          RKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    induced apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                211 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0924634
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                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.7%;
99.5%;
                                                                                                                                                         249
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Pred. No. 4.9e-105;
0; Mismatches 1;
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                                                                                                                                                                                                                                                       211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 5
AAY09369
ID AAYC
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AC AAYC
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DT 15-J
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DE Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             맒
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The TNF-related endothelium proliferative agent (TREPA), or its cativators or agonists, are used to treat a deficit of TREPA, e.g. to promote wound healing or tissue grafting, by promoting vascularisation, calso to induce apoptosis for treating cancer and eliminating autoreactive Treels, as an adjunct to cancer chemotherapy or antiviral treatment. TREPA peptides can also be used to target cytotoxic agents or for affinity isolation of the corresponding receptor, the nucleic acid for which can be used to transform tumour cells to render them more cresponsive to TREPA and to screen for TREPA mimics. TREPA-associated diseases, e.g. tumours and metastases (by inhibiting conditions involving abnormal stimulation of epithelial cells (e.g. atherosclerosis), for birth control (inhibiting ovulation and placental contraction) or other angiogenic conditions (e.g. ulcers).
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 199
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                                                           AAY09369;
                                                                                        AAY09369 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting nucleic acid encoding TREPA - useful for diagnosis treatment of autoimmune disease, tumours and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-447255/38
N-PSDB; AAV47613.
                              15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 16; Page 123-4; 142pp; English.
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12-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue grafting; vascularisation; apoptosis; autoimmune; birth control
                                                                                                                                                                206
                                                                                                                                                                                             182
                                                                                                                                                                                                                          146
                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                 88
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                           62 EQLVRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLR 121
                                                                                                                                                                                                                                                                                                                                          26 LGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL
                                                                                                                                                                                                                                                                                                                                                     2 LSLGLALACLGLLLVVVSLGSWATLSAQEPSQEELTAEDRREEPPELNPQTEESQDVVPFL
                                                                                                                                                               QLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH
                                                                                                                                                                                            QLRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH
                                                                                                                                                                                                                                     YDRQIGEETVIRAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGP 181
                                                                                                                                                                                                                                                                                YNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             249
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                           (first entry)
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97US-0798692
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                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                87.8%;
                                                                                                                                                                                                                                                                                                                                                                                              9;
                                                                                        249
                                                                                                                                                                                                                                                                                                                                                                                                  Score 1020; DB 19;
Pred. No. 9.5e-98;
9; Mismatches 16;
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                                                                                                                                                               249
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                                                                                                                                                                                                                                                                                                                                                                                                                               249;
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Q

Human tumour necrosis factor Apo-3 ligand protein sequence.

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useful for

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RESULT 6
AABO7526
ID AABO
XX AABO
AC AABO
XX AABO
C AABO
XX AABO
XX TWEA
KW TWEA
KW TWEA
KW TWEA
XX HOMC
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XX HOMC
XX WO2(
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Matches
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                                                                                                                            TWEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has cytostatic activity. Apo-3 ligand can be used to induce apoptosis in mammallan cancer cells, to induce NF-KappaB-dependent transcription to induce JNK/SAPK-dependent responses in mammallan cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
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10-OCT-1997;
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       WO200042073-A1
                                                                                                                                                                                                                                                             20-OCT-2000
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                                                                                                                                                                                                           Amino acid sequence
                                                                                                                                                                                                                                                                                                               AAB07526
                                                                                                                                                                                                                                                                                                                                                                 AAB07526 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH
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                                                                                                                            ( protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Apo-3 ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249
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                                                                                                                                                                                                                                                          (first
                                                                                                                            immunological disorder; immune response; infagent; autoimmune disease; organ transplant
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97US-0062037
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                                                                                                      disease;
                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                        of a
                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ils factor; Apo-3 ligand; lymphotoxin; apoptosis;
transcription; JNK/SAPK-dependent response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.8%;
88.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (a tumour
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                                                                                                                                                                                                        soluble recombinant human
                                                                                                      GVHD; lymphoid
                                                                                                                                                                                                                                                                                                                                                               249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1020; DB 20;
Pred. No. 9.5e-98;
9; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pitti
                                                                                                                                                                                                                                                                                                                                                               ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a human tumour necrosis factor
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                                                                                            organ transplant reject: cell malignancy; shock;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor) homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225
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                                                                                                                                                                                                        TWEAK
                                                                                                                                                      inflammation;
                                                                                                                                                                                                      protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249;
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                                                                                                      tumour
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RRESULT 7
AAY95338
ID AAY9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               describes a method for preventing or treating an immunological disorder and/or inhibiting an immune response in an animal. The method comprises administering a TWERK blocking agent. The method inappropriate expression and/or activity of TWERK. These disorders include autoimmune diseases, acute and chronic inflammation, organ transplant rejection, Graft-versus-Host disease (GVHD), lymphoid companies, septic and other forms of shock, loss of immune
                                                                                                                         PRO207; human; antitumour; tumour; therapy; cytostatic; breast cancer; ovarian cancer; renal cancer; colorectal cancer; uterine cancer; prostate cancer; lung cancer; bladder cancer; central nervous system cancer; melanoma; leukaemia; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Preventing and treating immune responses using modulators, antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, us treating e.g. inflammation and graft versus host disease -
                                                                            Homo
                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                               AAY95338
                                                                                                                                                                                                                                                                                                                                                                                                              AAY95338 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a TWEAK protein describes a method for preventing or treating an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-476036/41
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                                                                                                                                                                                                                                                                                                             25-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQLVRPRRSAPKGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL
                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199;
                                                                                                                                                                                                                                                        PRO207 antitumour protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ess (as seen in human immunodeficiency virus (HIV) and failure of the immune response to tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig 1;
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                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000WO-US01044
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Location/Qualifiers 1..40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45pp;
                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.8%;
88.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1020; DB 21
Pred. No. 9.5e-98;
                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
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Indels Length

0

Gaps

0

61

249

181

121 85

145

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08-MAR-1999
21-APR-1999
28-APR-1999
14-MAY-1999
20-JUL-1999
26-JUL-1999
15-SEP-1999
15-SEP-1999
               The present sequence is that of human antitumour protein PRO207, as deduced from a foetal kidney cDNA clone (see AAA49717). PRO207 shows amino acid sequence identity to tumour necrosis factor family members, especially human lymphotoxin beta (23.4%) and human CD40 ligand (19.8%). Mol.wt. is 27.216. A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell to PRO179, PRO327, PRO320, PRO219, PRO221, PRO221, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866 (see AAY95337-49), their agonists or chimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder and central nervous system cancer, melanoma and leukaemia. Methods for the recombinant
                                                                                                                                                                  Claim 19; Fig
                                                                                                                                                                                                                                                N-PSDB; AAA49717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
        system cancer, expression of t
                                                                                                                                                                                                 Novel composition to inhibit neoplastic cell growth or tumor in mammal comprises polypeptides PRO179, PRO207, PRO221, PRO324, PRO328, PRO301, PRO526, PRO362, PRO356,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                 Napier
                                                                                                                                                                                                                                                                                             Ashkenazi
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99US-0134287.
99US-0144758.
99US-0145698.
99WO-US21090.
99WO-US21547.
                                                                                                                                                                                                                                                                                            Goddard
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/note=
24..35
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41..249
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27..33
/note=
29..35
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99US-0130232
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45..51
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36..42
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10..14
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139..143
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121..127
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118..124
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                                                                                                                                                                                                                                                                                  Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "amidation"
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                                                                                                                                                                                                                                                                                            Godowski PJ,
         proteins are
                                                                                                                                                                                                                                                                                            Gurney
         also
        provided
                                                                                                                                                                                                                                                                                           AL,
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                                                                                                                                                                                                   r for treating
, PRO320, PRO219,
5, PRO509 or
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RESULT 8
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Best Local
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TREPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                        Claim
                                                                                                                                                                                                                                 Inducing angiogenesis in mammal at desired sites for promoting wound healing, by administering soluble fragment of extracellular domain of tumor necrosis factor related endothelium proliferative agent protein
                                                                                                                                                                                                                                                                                                                        WPI; 2001-280760/29
N-PSDB; AAD04350.
                                                                                                                                                                                                                                                                                                                                                                                      Wiley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                              (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-1997;
10-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  249
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98US-0021706
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Pred. No. 9
                                                                                                                                                                      English.
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proliferative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proliferative
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The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molecules particularly members of tumour necrosis factor (TNF) family molecules designated as TREPA (TNF related endothelium proliferative agent). Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis in human for promoting wound healing and for vascularising grafted

for successful

grafting

and to promote tissue

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RESULT 9
AAU86129
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Best Local S
Matches 199
                                                                                                                                                                                                                                     28-JUL-1999
17-AUG-1999
31-AUG-1999
01-SEP-1999
15-SEP-1999
30-NOV-1999
01-DEC-1999
01-DEC-1999
05-JAN-2000;
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11-MAR-1999;
11-MAY-1999;
02-JUN-1999;
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22-JUN-1999;
20-JUL-1999;
26-JUL-1999;
WPI;
                                                       Marsters
Watanabe
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                                                                                                                  Ashkenazi AJ,
                                                                                                                                                                             (GETH
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199; Conservative
                                                       SA,

    benign tumour; malignant tumour; lymphoid malignancy;
neuronal disorder; stromal disorder; blastocoelic disory
ry disorder; immune disorder; anglogenic disorder;

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99US-123972P
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99WO-US12252
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99US-144758P
99US-1445698P
99US-145698P
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                                                       Pan J,
Wood WI;
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                                                                                      Pan
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                                                                                                                  Goddard
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                                                                                Godowski PJ,
{ RM, Roy MA,
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Pred. No. 9.5e-98;
9; Mismatches 16;
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                                                                                   Gurney
Smith
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                                                                                                            Hillan KJ;
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RESULT 10
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                                                                         18-MAR-1997;
07-AUG-1996;
18-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angigenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
                                                                                                                                                                                                                                             TRELL; tumour necrosis factor related ligand; tnf; treatment; cancer; autoimmune disease; immune system; stimulation; suppr
                                                                                                                                                                                                                                                                                                                                                            AAW47525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                  (BIOJ )
                                                                                                                            07-AUG-1997;
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                                                                                                                                                                                                                                rejection
                                    BIOGEN INC
                                                                                                                                                                                                                                            autoimmune
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          JĽ,
                                                                                                                                                                                                                                                                                                                                                             standard;
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                                    GENEVA FACULTY MEDICINE
                                                                                                                                                                                                                                                                                  tumour
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                                                                        97US-0040820.
96US-0023541.
96US-0028515.
                                                                                                                            97WO-US13945
                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                  necrosis
                                                                                                                                                                                                                                                                                                            entry)
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88.8%;
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Pred. No. 9.
                                                                                                                                                                                                                                                                                  factor related ligand
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nes 16;
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WPI; 1998-145619/13

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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of human tumour necrosis factor related I ligand (TRELL). TRELL or active fragments can be included with a CC carrier in pharmaceutical compositions to treat cancer, autoimmune CC diseases or immune responses to tissue grafts, or to stimulate or CC suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening CC compositions for binding. Agents interfering with TRELL-receptor CC binding can also be screened for, can then be administered, optionally with interferon- gamma, to induce cell death or CC contionally with interferon- gamma, to induce cell death or CC treat, suppress or alter immune responses (especially involving human CC adenocarcinoma cells) involving a signal pathway between TRELL and its CC receptor. It's coding sequence can be used in gene therapy for CC TRELL-related disorders in mammals (especially humans), e.g. tumours, CC amounts of a vector, e.g. a virus comprising a gene encoding TRELL. CC It may also be of use in the preparation of prepare probes for can determine an attract, by the trees.
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Best Local
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                                                                         Omo
                                                                                                                        Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4; developmental abnormality; gestational abnormalitity; prostate cancer; APO6; APO8; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
                                              WO9911791-A2
                                                                                                           apoptosis; human.
                                                                                                                                                                                                       Human TNRL3 protein
                                                                                                                                                                                                                                         18-JUN-1999
                                                                                                                                                                                                                                                                       AAW93590;
                                                                                                                                                                                                                                                                                                         AAW93590 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                       241
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                                                                           sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR 180
                                                                                                                                                                                                                                                                                                                                                                                                      QLRLCQVSGLLPLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  YNRQIGEFIYTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP
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88.8%;
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ue grafts
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AAU03499 ID AAU(

AAU03499

standard;

Protein;

RESULT 12

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181

198

SSLRIRTLPWAHLKAAPFLTYFGLFQVH 225 SSLRIRTLPWAHLKAAPFLTYFGLFQVH

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208

XXX DXXX

26-SEP-2001

(first

entry)

TWEAK extracellular domain; tumour necrosis factor; TNF; angiogenesis;

TWEAK extracellular domain-containing fusion protein

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                                                                                                                                                          В
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                                                                                                                                                                                                                                                                                                                       molety. APO4 polypeptides are also useful for identifying selective CC binding agents, useful in diagnosis/treatment of disease by binding of agents to the polypeptide/active fragment which is extracellular, or cx expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/ active fragments are also useful for screening CC for agonists and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vivo or in vitro. APO polypeptides are all useful as immunogens for preparing antibodies. APO4 is also useful for diagnosis/treatment of developmental or gestational abnormalities. APO8 was transfected to human breast carcinoma cell line
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes isolated Tumor Necrosis Factor (TNF) family receptor polypeptides: APO4, APO6, APO6 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding apot 1 liked to a therapeutic
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 40; Fig 13A; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          developmental or gestational abnormalities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                               18 VSLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKGRKA 77
                                                                                                                                                          1 VSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKT 60
                                                                              RARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYYRQIGEFIVTRAGLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-205191/17.
DB; AAX23424.
  YLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPG
                                       YLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLLPLRPG
                                                                                                RPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRAGLY 137
                                                                                                                                                                                                                                        al Similarity
185; Conserv
                      induced apoptosis.
                                                                                                                                                                                                                                                                                                                       208
                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                     ΑĄ,
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                                                                                                                                                                                                                                                           81.8%;
88.9%;
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                                                                                                                                                                                                                                      Score 951; DB 20;
Pred. No. 1.1e-90;
B; Mismatches 15
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                                                                                                                                                                                                                                                                              Length 208;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                             angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease The disorders mediated by angiogenesis include ocular disorders the disorders mediated by angiogenesis include ocular disorders of human diseases. The disorders mediated by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinopaths, retinopathy of prematurity, neovascular ibroplasia, rubeosis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, benign tumours and preneplastic conditions, myocardial anglogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic conditions to the properties of the properties 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocular neovascularisation; diabetic retinopathy; neovascular glaucom retinoblastoma; retinopathy of prematurity; retrolental fibroplasia; rubcosis; uveitis; macular degeneration; arthritis; rheumatism; corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joi malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in the isolation of human TWEAK receptor (TWEAKR)-expressing clones from a COS cell human cDNA library. The TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents a a fusion protein encoded by the expression vector pDC409-L2-TWEAK. The fusion protein comprises a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac peripheral tissue, by administering antagonist or agonist of TWEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-DEC-1999;
10-MAY-2000;
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                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                  atherosclerosis, peripheral atherosclerosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth hormone leader,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wiley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                               plaque neovascularisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 41; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-DEC-2000; 2000WO-US34755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IMMV ) IMMUNEX
127
                                                                                                         67
                                                                                                                                                                                                                                            Local
                                                79
                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extracellular domain
                                                                                                                                   SLGSWATLSAQEPSQEELTAEDRREPPELNPQTEESQDVVPFLEQLVRPRRSAPKGRKAR
                         PRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRAGLYY 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-417975/44
DB; AAS03964.
ARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYY
                                                                                                         SLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTR
                                                                                                                                                                                                                        184;
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                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                               273 AA;
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                                                                                                                                                                                                                                            81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a leucine zipper multimerisation domain, in of human TWEAK. The fusion protein was
                                                                                                                                                                                                             score 951; DB Pred. No. 1.6e 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               telangiectasia, wound granulation,
                                                                                                                                                                                                                                            DB 22;
                                                                                                                                                                                                                                                                                                                                                                                     ischaemia
                                                                                                                                                                                                                                                                      Length
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186
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                                                                                                                                                                                   The TNF-related endothelium proliferative agent (TREPA), or its cativators or agonists, are used to treat a deficit of TREPA, e.g. to promote wound healing or tissue grafting, by promoting vascularisation, calso to induce apoptosis for treating cancer and eliminating autoreactive reclis, as an adjunct to cancer chemotherapy or antiviral treatment. TREPA peptides can also be used to target cytotoxic agents or for caffinity isolation of the corresponding receptor, the nucleic acid for which can be used to transform tumour cells to render them more cresponsive to TREPA and to screen for TREPA mimics. Treatment to TREPA and to screen for TREPA mimics. TREPA-associated diseases, e.g. tumours and metastases (by inhibiting conditions involving abnormal stimulation of epithelial cells (e.g. atherosclerosis), for birth control (inhibiting ovulation and placental condition) or other angiogenic conditions (e.g. ulcers).
                                                                                                     Matches
                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNF; endothelium proliferative agent; TREPA;
tissue grafting; vascularisation; apoptosis;
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting nucleic acid encoding TREPA - useful for diagnosis treatment of autoimmune disease, tumours and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-447255/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wiley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-1998;
12-FEB-1997;
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133 RAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLL 192
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                                                                                                                  Local
                                           37
                                                         73 KGRKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLRIRTLPWAHLKAAPFLTYFGLFQVH
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                                           KGRKTRARRGIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGS
                                                                                                   al Similarity
142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                              Page 125-6; 142pp; English.
                                                                                                                                                              189
                                                                                                     Conservative
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97US-0798692.
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                                                                                                                  63.9%;
92.8%;
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                                                                                                                  Score
Pred.
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                                                                                                                  742; DB 19;
No. 5.7e-69;
                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               wound healing; cancer; autoimmune; birth cont
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                                                                                                                              Length 189;
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RESULT 14
AAEOU892
ID AAEOU
XX AAEOU
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XX Human
XX Human
XX TREPP
KW Vulne
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                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soluble biologically active TREPA are used to treat TREPA associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis in human for promoting wound healing and for vascularising grafted tissue for successful grafting and to promote tissue grafts. The present amino acid sequence is human UL4flag TREPA soluble construct. This sequence which is a biologically active molecule is capable of inducing proliferation in HUVEC (human umbilical vein endothelial cells) cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molecules designated as TREPA (TNF related endothelium proliferative agent).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Inducing angiogenesis in mammal at desired sites for promoting wound healing, by administering soluble fragment of extracellular domain of tumor necrosis factor related endothelium proliferative agent protein
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10-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Column 75-78;
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                                                        193
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                                                                                                           97
                                                                                                                                                                                                                    PLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
                                                  PLRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH 225
                                                                                                                                      RAGLYYLYCQVHFDEGKAVYLKLDLLVNGVLALRCLEEFSATAASSPGPQLRLCQVSGLL 192
ALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH
                                                                                                           RAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLL
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142; Conserv
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                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
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98US-0021706.
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                                                                                                                                                                                                                                                                                                                                                                    63.9%;
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                                                                                                                                                                                                                                                                                                                                            Mismatches
189
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RESULT 15
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molecules designated as TREPA (TNF related endothelium proliferative agent). Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis in human for promoting wound healing and for vascularising grafted tissue for successful grafting and to promote tissue grafts. The present amino acid sequence is human TREPA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human;
TREPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inducing angiogenesis in mammal at desired sites for promoting wound healing, by administering soluble fragment of extracellular domain of tumor necrosis factor related endothelium proliferative agent protein
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10-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human TREPA (TNF related endothelium proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE00895 standard; Protein;
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121
                                                                                                                                                               140
                                                                                                                                                                                                                 61
                                                                                                        LRIRTLPWAHLKAAPFLTYFGLFQVH 146
                             LRIRTLPWAHLKAAPFLTYFGLFQVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SR;
                                                                                                                                                                                                                                                                                                                                  138;
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                                                AUTHORS
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ALIGNMENTS

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DEFINITION
Mus musculus adult retina CDNA, RIKEN full-length enriched library, clone:A930030D13:tumor necrosis factor (ligand) superfamily, member 12, full insert sequence.
ACCESSION
AK020909
AK020909.1 GI:12861640
KEYWORDS
SOURCE
Clone_lib:RIKEN full-length enriched mouse cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
clone=A330030D13.

ORGANISM
Mus musculus
Clone_lib:RIKEN full-length enriched mouse cDNA library
clone=A390030D13.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
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10349636
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AUTHORS
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
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JOURNAL
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Genome Res. 10 (10), 1617-1630 (2000)

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
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Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Araikam, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Sohrimi, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tejama, Y., Tayami, M., Tagawa, A., Takahashi, F., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
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cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GACAGACAGGATCCAAGAGCTCTTTTTTTTTTTTTTTN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through two rounds of normalization to Rot = 20.0 and subtraction to Rot = 458.8. Second strand cDNA was prepared with the primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 30-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gratefully acknowledged.
Retina RNA was provided by Stefano Gustincich (Department
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/dev_stage="adult"
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                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9767 row: p column: 20
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Rodentia;
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/lab_host="DH10B (T2 phage=resistant)"
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Site_2: SalI; Cloned unidirectionally. Pr
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mRNA sequence. B1871711 B1871711.1 GI

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Craniata; Vertebrata; Catarrhini; Hominidae;

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CCTCCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTACTTTGGACTCTTTCAAGT
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                                                                                                                                                                    CTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGGC
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Tissue Procurement: ATCC
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Plate: LLAM12034 row: b column: 07
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Contact: Robert St
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1.
Site_2: SalI; Cloned unidirectionally; oligo-dT |
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Techno Note: this is a NIH_MGC Library."
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/clone="IMAGE:5405478"
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Pred. No. 3.4e-124;
0; Mismatches 101;
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Best Local
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               AGCCCATTATGAGGTTCATCCTCGGCCAGGACAGGATGGAGCACAAGCAGGTGTGGATGG
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CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM12034 row: a column: 12 High quality sequence stop: 728.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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1 (bases 1 to 728)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/lab_host="DHIOB (phage=resistant)"
/note="Organ: liver; Vector: pCwV-SPORT6; Site_1: Noti;
Site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."

a 240 c 227 g 136 t
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/db_xref="taxon:9606"
/clone="IMAGE:5405459"
/clone_lib="NIH_MGC_90"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 561)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Projection
                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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ur70d09.yl NCI_CGAP_Mam3 Mus
similar to TR:054907 054907 :
                                                                                                                                       Seq p
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Other_ESTs: ur70d09.x1
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house mouse
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                                                                                                                     quality sequence stop:
Location/Qualifiers
/organism="Mus musculus"
/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3155633"
/clone_11b="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
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REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 6 BE628951 rocus DEFINITION JOURNAI BE628951 533 bp mRNA linear EST 25-AUG-2000 uu30c03.yl Soares_mammary_gland_NMLMG Mus musculus cDNA clone IMAGE:3373444 5' similar to TR:054907 O54907 TNF-RELATED WEAK Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 533) Unpublished (1997)
Contact: Robert Strausberg, Ph.D. Mus musculus EST Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL ; Tumor Gene Index National Cancer Institute, NCI-CGAP http://www.ncbi.nlm house mouse BE628951.1 INDUCER OF MGI:1083048 [MAGE Consortium (info@image.llnl.gov) APOPTOSIS ;, GI:9911639 mRNA sequence. Cancer .nih.gov/ncicgap Genome for Anatomy further information Project (CGAP), contact the

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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. " as 206 c 105 g 131 t
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/clone="IMAGE:3373444"
/clone_11b="Soares_mammary_gland_NMLMG"
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/tissue_type="mammary gland"
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                                         GCTGCTCCTTGGTCCAGTCCTGT-CTCTCCTCAAAGGCAGCCCAGAGCTTGTTCACATGTT
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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National Institutes of Health, N
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plate: LLAM10435 row: h column: 15
High quality sequence stop: 468.
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/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
/notice="organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;

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92.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No. 1.9e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ208433
BQ208433.1
EST.
Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Feax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized duodenum library cDNA Library Preparation: M.B. Soares
Lab Clone distribution: clones will be available through Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EQ208433 687 bp mRNA UI-R-EP0-coc-1-22-0-UI.s1 UI-R-EP0 Rattus UI-R-EP0-coc-1-22-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics (www.resgen.com)
Seq primer: M13 Forward
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                                                                                                  165
                                                                                                                                                                                                                                 /lab_host="NHOB" (Life Technologies)"
/lab_host="NHOB" (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; UI-R-EPO is a
subtracted cDNA library constructed according to Bonaldo,
Lennon and Soares, Genome Research, 6:791-806, 1996. First
strand cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tags for this
library are: distal colon, GAAGTGCTCC; osteoblast,
AAGATATCAA; cell line R3327 5A, GGACTAAGTC; cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                      TAG_LIB=UI-R-EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="ADULT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="UI-R-EP0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="UI-R-EPO-coc-1-22-0-UI
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                                                                                           G_TISSUE-duodenum

NG_SEQ=TGTGGTTCAT"

139 C 219 9
41.8%;
87.9%;
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Rodentia;
Score 488.8; DB 14; Pred. No. 3.1e-116;
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Sciurognathi; Muridae;
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RESULT 9
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                                                                                                                                                                                                                 EST348878 Rat gene index, normalized rat, norvegicus, Rattus norvegicus cDNA clone RGIEF49 5' end, mRNA sequAW917574
               Contact: Lee,
The Institute
                                         Unpublished (1998)
                                                                                Lee, N.H., Glodek, A.,
Kerlavage, A.R. and Ac
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                            Norway rat.
Rattus norvegicus
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                                                                                                                        Rattus
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                                                                   Genome Project:
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nstitute for Genomic Research
Medical Center Drive, Rockvi
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BI819200
BI819200.1
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Fax: (301)-838-0208
Email: nhiee@tigr.org
This clone is available through the ATCC,
tel#703-365-2700 for further information
                       BI819200
603034614F1 NIH_MGC_115
mRNA_sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pBlueScript SK(-); Site_1:
Xho1; Estimated insert size approx.1 kb"
188 c 147 g 138 t 3 others
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Bento Soares"
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/db_xref="taxon:10116"
/clone="RGIEF49"
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/lab_host="SOLR"
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liver, embryo, heart, muscle, spleen"
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91.3%;
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Pred. No. 2.8e-114;
0; Mismatches 46;
                                     Homo
                                    sapiens
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                                                    CTGGTGAACGGTGTGCTGGCCTGCGCTGCCTGGAAGAATTCTCAGCCACAGCAGCAGC
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TCTCCTGGGCCCCAGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGGCTGCGGCCAGGG
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cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln1.gov
Plate: LLAM11437 row: 1 column: 03
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 777)
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:5175698"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
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81.6%;
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Pred. No. 5.1e-114;
0; Mismatches 126;
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B1766766
B1766766.1 GI:
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 834)
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National Institutes of Health, Mammalian
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                       154
                                                    (Invitrogen).
this is a NIH_
a 287 c 2
                                                                                                               /note=*Organ: pooled lung and spleen; Vector: pcMV-SPORT6 Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size
                                                                                        range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber
                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                    /clone="IMAGE:5206217"
/clone_lib="NIH_MGC_122"
                                                                                                                                                                                             /lab_host="DH10B"
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primatės; Catarrhini; Hominidae;
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2466 row: n column: 17
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Tissue Procurement: Dr. Mark Watson
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Contact: Robert Strausberg, Ph.D.
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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Secort; cDNA made by oligo-dT priming. Directionally
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/clone="IMAGE:6278608"
/clone_lib="NIH_MGC_113"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Tissue procurement: Miklos Pakkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.N.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                              http://image.llnl.gov
Plate: LLAM11722 row: k column:
High quality sequence stop: 776.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
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National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 828)
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                                                                                                                                                  /clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:5285892"
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                39.1%;
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Score 456.4; DB 13;
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0; Mismatches 106;
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AA221610
AA221610.1 GI:1840863
                                                                             Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 471)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.
         Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
                                                        The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                     house mouse.
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5', mRA sequence.
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334 GACCAAAATCAACAGCTCCAGCCCTCTGCGCTACGACCGCCAGATTGGGGAATTTACAGT
            GGCTGCCCCCTTCCTAACCTTTGGACTCTTTCAAGTTCACTGAGGGGCCCTTGCTC
                                                                                                          GTTGCCGCTGCGGCCAGGGTCTTCCCCTTCGGATCCGCACCCTCCCCCTGGGCTCATCTTAA
                                                                                                                                           CCAGATTCCTTAAACTTTCCCTGGCTCCAGGAGCATCACCACACCTCCCTA 471
                                              GGCTGCCCCCTTCCTAACCTACTTTGGACTCTTTCAAGTTCACTGAGGGGCCCTTGCTCTC
                                                                                               GTTGC - -GCTGCGGCAGGGTCTTCCCTTCGGATCCGCACCCTCCCCTGGGCTCATCTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:429769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -28m13 rev2 ET from Amersham
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57; Conservative
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Location/Qualifiers
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/db xrof-"
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/clone_lib="Barstead mouse
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCN2456 row: 1 column: 13
High quality sequence stop: 565.
LCcation/Qualifiers
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NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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human.
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Tissue Procurement: ATCC
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Contact: Robert St
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Eukaryota; M
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/lab_host="pH10B (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5 adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
a 326 c 260 g 183 t
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/clone="IMAGE:6274716"
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Eutheria; Primates;
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78.5%;
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Pred. No. 1.2e-98;
0; Mismatches 144;
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Search completed: March 31, 2003, 11:47:15 Job time: 2156.97 secs

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Database
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Human gene express	Primer used in the	Listeria monocytog	2	Gene encoding a su			Oligonucleotide fo			~	M. tuberculosis re			Oligonucleotide fo	Listeria monocytog	Human DNA for a no	DNA f	CDNA	Human cDNA clone (Human metastasis a	Human immune syste	Chemically treated		Human gene express	DNA encoding endot		poly			Mouse spliced tran	Colon adenocarcino	Human gene signatu	Expression vector	Human TNRL3 DNA.

ALIGNMENTS

RESULT 1 AAV18599 18-MAR-1997; 07-AUG-1996; 18-OCT-1996; TRELL; tumour necrosis factor related ligand; tnf; treatment; cancer; autoimmune disease; immune system; stimulation; suppression; graft rejection; ds. Key (BIOJ) BIOGEN INC. 07-AUG-1997; WO9805783-A1 Mus musculus Mus musculus tumour necrosis factor related ligand (TRELL) gene. 21-JUL-1998 (first entry) AAV18599; AAV18599 standard; cDNA; 1168 BP 12-FEB-1998. 97US-0040820. 96US-0023541. 96US-0028515. 97WO-US13945 Location/Qualifiers 2..679 /*tag= /note= "tumour necrosis factor related ligand"

GENEVA FACULTY MEDICINE

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CGGTGTGCTGGCCCTGCGCTGCCTGGAAGAATTCTCAGCCACAGCAGCAAGCTCTCCTGG
                                                                       CTGTCAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGAA
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DB; AAW47524.
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Pred. No. 8.2e-307;
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11-MAR-1999

04-SEP-1998;

98WO-US18393.

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CC receptor polypeptides: APO4, APO8 and APO9 or their active CC fragments, and isolated TWF related ligands I and 3 (TMRLI and TMRL3) or CC their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 in an individual. Prostate cancer CC by determining levels of APO4 in an individual. Prostate cancer CC molety. APO4 polypeptides are also useful for identifying selective CC molety. APO4 polypeptides are also useful for identifying selective CC binding agents, useful in diagnosis/treatment of disease by binding of CC expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/active fragments are also useful for screening CC for agonists and antagonists by binding and observing the changer in APO4 CC activity. Effective pharmacological agents useful in diagnosis or CC treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vivo or in vitro. APO polypeptides CC useful for diagnosis/treatment of developmental or gestational CC abnormalities. APO8 was transfected to human breast carcinoma cell line CC abnormalities. APO8 was transfected to human breast carcinoma cell line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 701
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DB; AAW93591.
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99.9%;
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Pred. No. 1.1e-179;
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08-MAR-1999;

21-APR-1999;

28-APR-1999;

14-MAY-1999;

20-JUL-1999;

26-JUL-1999;

15-SEP-1999;

15-SEP-1999;
                                                                                          P-PSDB;
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Napier MA, Pitti RM,
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breast cancer;
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DB; AAY95338.
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                                                                                                                                                                                                                       ) GENENTECH INC.
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99WO-US05028.
99US-0130232.
99US-0131445.
99US-0144758.
99US-0146578.
99US-0145598.
99WO-US211990.
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58..177
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Novel composition to inhibit neoplastic cell growth or tumor in mammal comprises polypeptides PRO179, PRO207, PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356,

for treating PRO320, PRO219, , PRO509 or

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                                   CTCTTTCAAGTTCACTGAGGGGCCTTGCTCTCCCAGATTCCTTAAACTTTCCCTGGCTCC
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pred. No. 2.5e-160;
0; Mismatches 219;
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cDNA;

entry)

human PRO207 polypeptide

Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disorderlammatory disorder; immune disorder; anglogenic disorder; gene therapy; cytostatic; neuroprotective; gene; ss. disorder;

2000WO-US03565

99US-123972P.
99US-133459P.
99WO-US12252.
99US-140650P.
99US-140653P.
99US-145698P.
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30-NOV-1999;
01-DEC-1999;
01-DEC-1999;
05-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABK40254-ABK40288 encode for the human PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi AJ,
Marsters SA,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 50; Fig 3; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
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DB; AAU86129.
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; 99WO-US28313.
; 99WO-US28301.
; 99WO-US28634.
; 2000WO-US00219.
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76.2%;
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Pred. No. 2.5e-160;
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10-OCT-1997;
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                                                                                                                                     TGTCAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAAC
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                                          CCCCAGCTCCGCCTCTGCCAGGTGTCTGGGCCTGTTGGCCCTGCGGCCAGGGTCCTCCCTG
                                                                                 GGTGTGCTGGCCTGCCTGCAGGAAATTCTCAGCCACTGCGGCGAGTTCCCTCGGG
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97US-0062037
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08-MAY-2002 ABK34881; ABK34881 standard; (first cDNA; entry) 1364 ВP

Human cDNA encoding secreted

protein

#19.

RESULT 6
ABK34881
ID ABK3
XX ABK3
AC ABK3
XX DT 08-M
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DE Huma
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DE Huma
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PD 18-(
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XX 29-1
XX (GE1 Human; secreted protein; gene; ss; nutritional supplement; haemophilia; viral infection; bacterial infection; fungal infection; diabetes; asthmu autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour; autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer. coagulation disorder; inflammatory disorder; Crohn's disease; incision; tissue regeneration; wound healing; burn; haematopolesis; myeloid cell deficiency; lymphoid cell deficiency asthma;

Homo sapiens

WO200177288-A2

18-0CT

29-MAR-2001; 2001WO-US10224

06-APR-2000; 2000US-195582P

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CC Sequences ABK34863-ABK35454 represent polynucleotides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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 CCCCAGCTCCGTTTGTGCCAGGTGTCTGGGCTGTTGCCGCTGCGGCCAGGGTCTTCCCCTT
                          TGTCAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAAC
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Similarity 76.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilgand (TRELL). TRELL or active fragments can be included with a carrier in pharmaceutical compositions to treat cancer, autoimmune diseases or immune responses to tissue grafts, or to stimulate or suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for, can then be administered, optionally with interferon- gamma, to induce cell death or treat, suppress or alter immune responses (especially involving human adenocarcinoma cells) involving a signal pathway between TRELL and its receptor. The DNA sequence can be used in gene therapy for TRELL-related disorders in mammals (especially humans), e.g. tumours, by introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL. It may also be of use in the preparation of prepare probes for screening natural/synthetic DNAs for TRELL-encoding sequences
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Best Local S
Matches 906
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07-AUG-1996;
18-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1373 BP; 247 A; 462 C; 394 G;
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              CGCTACGACCGCCAGATTGGGGGAATTTACAGTCATCAGGGCTGGGCTCTACTACCTGTAC
                                                                  GGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCCTCTG
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DB; AAW47525.
                                                                                                                                                            CTGAACCGACTAGTTCGGCCTCGCAGAAGTGCACCTAAAGGCCGGGAAAACACGGGCTCGA
                                                                                                                                                                          TTGGAACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAGGCCGGAAGGCGCCGCCTCGC
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CGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACCTGTAC
                                                    GGTGTGGACGGGACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTG
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UNIV GENEVA FACULTY MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 1.6e-156;
0; Mismatches 219;
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                                                                                      TNF; endothelium proliferative agent; TREPA; wound healing;
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                                                                             grafting;
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                                                                                                          endothelium proliferative agent
                              Location/Qualifiers
1..750
                                                                              vascularisation;
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                                                                              apoptosis; autoimmune;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 879;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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12-FEB-1997;
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TGTCAGGTGCACCTTTGATGAGGGGAAAGGCTGTCTACCTGAAGCTTGGACTTGCTGGTGAAC
                                                            CGCTACGACCGCCAGATTGGGGAATTTACAGTCATCAGGGCTGGGCTCTACTACCTGTAC
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                                                                                                                                   Human; tumour necrosis factor; TNF; angiogenesis; wound healing;
TREPA; TNF related endothelium proliferative agent; tumour; meta
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                                                                                             Homo sapiens
                                                                                                                     grafting; vulnerary;
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                                                                                                                                                                         TREPA (TNF related endothelium proliferative agent) cDNA.
                                                                                                                                                                                                   (first entry)
  /*tag= a
/product= "Human TREPA (TNF related endothelium
proliferative agent)"
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Best Local S
Matches 879
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10-FEB-1998;
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DB; AAE00891.
                                                       TGTCAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAAC
                                                                                                   GGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGACCAAAATCAACAGCTCCAGCCCTCTG
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                                             TGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGAT
                                                                                         CGCTACAACCGCCAGATCGGGGAGTTTATAGTCACCCGGGCTGGGGCTCTACTACCTGTAC
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75.2%;
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                                    W09911791-A2
                                                                                                                                         apoptosis; human;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 643; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Tumor Necrosis Factor family receptor polypeptides and useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
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81.6%;
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Pred. No. 1.2e-131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   corneal graft neovascularisation; psoriasis; metastatic condition; malignant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TWEAK extracellular domain; tumour necrosis factor; TNF; anglogenesis; ocular neovascularisation; diabetic retinoplath; neovascular glaucoma; retinoblastoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; ds;
                                                                                                                                                                        19-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                              "Fusion protein comprising a growth hormone leader, a leucine zipper multimerisation domain, and human TWEAK extracellular domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the isolation of human TWEAK receptor (TWEAKR) expressing clones from a COS cell human cDNA library. The TWEAK protein is a member of the tumour necrosis factor (TMP) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, necessional and metastatic conditions such as ascorbased as a conditions such as archaeled diseases include mallignant and metastatic conditions such as archaeled according tumours and prepared to conditions such as archaeled according tumours and prepared to conditions such as archaeled according to the conditions and prepared to conditions such as archaeled according to the conditions and prepared to conditions such as archaeled according to the conditions and prepared to conditions such as archaeled according to the conditions and prepared to conditions according to the conditions and prepared to conditions and prepared to conditions according to the conditions and prepared to conditions and the conditions are conditions as archaeled according to the conditions and the conditions and the conditions and the conditions archaeled according to the conditions and the conditions archaeled according to the conditions and the conditions and the conditions archaeled according to the conditions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic plaque neovascularisation, telanglectasia, wound granulation, coronary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac or peripheral tissue, by administering antagonist or agonist of TWEAK
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CCTGGGCCCCAGCTCCGTTTGTGCCAGGTGTCTGGGCCTGTTGCCGCCTGCGGCCAGGGTCT
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DB; AAU03499.
                                                        GTGGATGGTGTGCTGCCCTGCGCTGCCTGGAGGAATTCTCAGCCACTGCGGCCAGTTCC
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87.0%;
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                                                                                                                                                                 A single-stranded DNA (or its complementary strand or the corresp. C double-stranded DNA) which comprises one of the 7837 "GS" sequences given in AAT19001-T26837 and which is able to hybridise to part of human genomic DNA, CDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'- untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for recognising different cell types.
                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MATS/)
(OKUB/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene signature HUMGS03761.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 1067; 2245pp; Japanese.
                                                                                                                      282 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ng; mapping; non-blased library; dlagnosis; cabnormal cell function; ss.
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                                                                                                                      80 A; 62 C;
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Pred. No. 1.9e
0; Mismatches
                                                                                                                      69 G; 66
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               The invention relates to an isolated polynucleotide (I) encoding a CC polypeptide (II) comprising a portion of a colon tumour protein. A new CC oligonucleotide (III) that hybridises to (I) is useful for CC expanding the presence of a cancer in a patient. (II) or antigen CC expanding T cells expressing (I) are useful for stimulating and/or CC expanding T cells specific for a tumour protein, by contacting T cells (II), or antigen presenting cells that express (II) are useful for treating CC colon cancer in a patient by incubating CD4+ and/or CD8+ T cells isolated CC from a patient with (I), (II), or antigen presenting cells that express (II) are useful for the patient an CC effective amount of the proliferate, and administering to the patient an CC effective amount of the proliferated T cells, thus inhibiting the CC colon cancer in the patient. A new composition is useful in Vaccines and pharmaceutical compositions for prevention and treatment of CC colon cancer and for the diagnosis and monitoring of the cancers. (I), CC (II) or an antibody against (II) is useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of ribozyme CC molecules for inhibiting expression of (II) in tumour cells. ABK29475-
CC ABK29551 represent human colon adenocarcinoma-specific cDNA sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
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22-NOV-2000;
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RESULT 14
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        set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue- and patholog-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABNN7253 to ABN59589 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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                                                                                                                                                                                                                                   transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively
                                                                                                                                                                                                                                                                                                                                Example 1;
                                                                                                                                                                                                                                                                                                                                                                           New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription a genome, useful for detecting tissue-, pathology-, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shoshan A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-2000; 2000US-221607P
02-MAY-2001; 2001US-287724P
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                                                                                                                                                                                                                                                                                 messenger RNAs that populate a (sub-)transcriptome, where
                                                                                                                                                                                                                                                                                                 The present invention describes oligonucleotide libraries for detecting
                                                                                                                                                                                                                                                                                                                                                              developmental-specific
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                                                                                                                                                                                                                                                                  (sub-)transcriptome comprises messenger RNAs transcribed from multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (COMP-) COMPUGEN INC
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variant; transcriptome; oligonucleotide library; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcript detection oligonucleotide SEQ ID NO:28723
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RESULT 1:
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having a sequence that selectively hybridises to a PKD1 gene sequence and optionally, to a PKD1 homologue sequence and an adjacent 3' region having a sequence that selectively hybridises to a PKD1 gene sequence and not to a PKD1 homologue sequence. Primer pairs of the invention are useful for detecting the presence or absence of a mutation in a PKD1 polynucleotide in a sample, for identifying a subject at risk for a PKD1-associated disorder such as autosomal dominant polycystic kidney disease (ADPKD) or acquired cystic disease and for diagnosing a PKD1-associated disorder in a subject. They are useful for selectively amplifying a region of a PKD1 gene. PKD1 DNA fragments are useful detecting the presence of a mutant PKD1 polynucleotide in a sample, amplification assays of biological samples to detect abnormalities of PKD1 expression and for engineering transgenic animals. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                          The present invention relates to compositions and methods useful for the identification and detection of polycystic kidney disease (PKD1) gene mutations. The invention also relates to primers comprising a 5' region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the exemplification of the present invention.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; PKD1 gene; autosomal dominant polycystic kidney disease; acquired cystic disease; transgenic animal; chromosome 16; ds.
                                                                                                                                                                                                                                                                                                             Claim 20; Page 127-156; 192pp; English.
                                                                                                                                                                                                                                                                                                                                          disorder, comprises regions having sequence to polycystic kidney disease gene sequence
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13-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                            primer for diagnosing polycystic kidney disease-associated der, comprises regions having sequence that selectively hyb
                                                                                                                                                                                                                                                                                                                                                                                                                                                    GG,
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48.7%;
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LOCUS	AF030100	1168 bp mRNA	mRNA	linear	ROD	ROD 20-DEC-1997
DEFINITION	DEFINITION. Mus musculus TWEAK mRNA, partial cds.	, partial	cds.			
ACCESSION	AF030100					
VERSION	AF030100.1 GI:2707220					
KEYWORDS	•					
SOURCE	Mus musculus.					
ORGANISM	Mus musculus	•				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	rdata; Cra	miata; Ve	rtebrata;	Eute	leostomi;
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	entia; Sci	urognathi	; Muridae	; Mur	inae; Mus.
REFERENCE	1 (bases 1 to 1168)					
AUTHORS	Chicheportiche, Y., Bourdon, P.R., Xu, H., Hsu, Y.M., Scott, H.,	don, P.R.,	Xu, H., Hs	u, Y.M., So	ott,	H.,
	Hession, C., Garcia, I. and Browning, J.L.	nd Brownin	g,J.L.			6
TITLE	TWEAK, a new secreted ligand in the tumor necrosis factor family	igand in t	he tumor	necrosis	racto	r ramily

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/db_xref="GI:2707221"
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DGTVSGWEETKINSSSFLRYDROIGEFTVIRAGLYYLYCQVHFDEGKAVYLKLDLLVN
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Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
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Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,
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Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,
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Perez, L., Relter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D. M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
Worley, K., and Gibbs, R.
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Mammalia; Eutheria; Rodentia;
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chemistry: Dye-primer Bodipy: 48% of reads Chemistry: Dye-terminator Big Dye: 52% of reads Assembly program: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 212648 bases at least Q40
Consensus quality: 218902 bases at least Q30
Consensus quality: 222384 bases at least Q20
Estimated insert size: 210656; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 7.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: MAFO
Center clone name: Rp23-168p5
------ Summary Statistics
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy:
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62253
118773
1118873
144925
149025
167232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="11"
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62352: gap of unknown length
118772: contig of 56520 bp in length
118872: gap of unknown length
1148924: contig of 30052 bp in length
149024: gap of unknown length
167231: contig of 18207 bp in length
167331: gap of unknown length
167331: gap of unknown length
189907: contig of 22576 bp in length
199007: gap of unknown length
190007: gap of unknown length
190637: contig of 6300 bp in length
196637: gap of unknown length
196637: gap of unknown length
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Pred. No. 2.5e-176;
D; Mismatches 0;
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                                                                                                                                                    Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enguiries:
humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk
On Nov 20, 2001 this sequence version replaced gi:16605765.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete sequence AL603707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL603707 234182 bp DNA linear ROD 17-Mouse DNA sequence from clone RP23-422L16 on chromosome 11,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pearce, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
1. .234182
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/clone_lib="RPCI-23"
complement(84050. .84131)
complement(84050. nd-directional primer
/note="Sequence from uni-directional primer
big dye terminator reads only."
a 56824 c 57519 g 60529 t
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/db_xref="taxon:10090"
/chromosome="11"
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Pred. No. 2.6e-176;
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          CCCCAGCTCCGTTTGTGCCAGGTGTCTGGGGCTGTTGCCGCTGCGGCCCAGGGTCTTCCCTT
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Ashkenazi, A.J., Goddard, A., Godowski, P.J., Gurne
Hillan, K.J., Marsters, S.A., Pan, J., Pitti, R.M.,
Stone, D.M., Watanabe, C.K. and Wood, W.I.
Compositions and methods for the treatment of tu
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="taxon:9606"
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                                                          Curr. Biol.
98228355
9560343
Ashkenazi,A.

Direct Submission
Direct Submission
Submitted (25-MAR-1998) Moles
South San Francisco, CA 9408
Location/Qualifiers
                                                                                                                                                                         1368
Homo sapiens Apo3/DR3 ligand
AF055872
                                                                                    Apo3
                                        2 (bases 1 to Marsters, S.A.,
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                                                                                                   Ashkenazi,A
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Sheridan,J.P.,
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                                          Pitti,R.M.,
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CTCTTTCAAGTTCACTGAGGGGCCTTGCTCTCCCAGATTCCTTAAACTTTCCCTGGCTCC
                                                           CGGATCCGCACCCTCCCCTGGGCTCATCTTAAGGCTGCCCCCCTTCCTAACCTACTTTGGA
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                                        CGGATCCGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCCTTCCTCACCTACTTCGGA
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/chromosome="17"
/map="17p13"
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/function="binds to
Apo3/DR3"
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ARRAIAHAYEVHPREGGDAQAGVGDTVSGWEBARTNSSSGFLKYNRQIGEATYNGAGTAGL
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/organism="Homo sapiens"
/ar vraf="taxon:9606"
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Pred. No. 7.6e-155;
0; Mismatches 219;
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                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata Mammalla; Eutheria; Primates; Catarrhini; Hominida 1 (bases 1 to 1306) Chicheportiche, Y., Bourdon, P.R., Xu, H., Hsu, Y.M., Hession, C., Garcia, I. and Browning, J.L. TWEAK, a new secreted ligand in the tumor necrosis
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Cambridge, MA 02142, USA
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/map="17p13"
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          /tissue_type="tonsil"
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Sequence 1 :
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RESULT 8 AC119115 LOCUS

DEFINITION

AC119115

138792 bp DNA s clone CH230-320N23, d pieces.

DNA

SEQUENCING linear

HTG

PROGRESS 18-JUL-2002

ACCESSION VERSION

Rattus norvegicus (
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AC119115
AC119115.2 GI:2174

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KEYWORDS SOURCE

HTG; HTGS_PHASE1.

GI:21746718

ORGANISM

Norway rat. Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata;

Vertebrata;

Euteleostomi;

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REFERENCE AUTHORS

Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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Earnhart.C., Edgar,D., Edwards,C.C., Elhaj.C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcla,A., Garner,T., Garza,N., Gill,R., Gabisi,A., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Halliton,K., Harris,C., Harris,K., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karisson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucler,R., Luna,R., Ma,J., Mansey,E., Mawhiney,E., McLeod,M.P., Meator,M., Me1,G., Metzker,M., Mapus,P., Martin,R., Martindale,A., Martinez,E., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S., Moser,N., Noyledo,R., Pace,A., Payton,B., Oguh,M., Okwuonu,G., Oragunye,N., Ovledo,R., Pace,A., Payton,B., Deerey,J., Perez,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Sten,H., Shooshtari,N., Sisson,I., Soherer,S., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Shonshtari,N., Vinson,R., Wang,O., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlinamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,Y., Wu,Y., E., Shou,J., Zorrilla,S., Nelson,D., Welson,D., Welson,D., Shou,J., Shou,J., Sondiky, Shou,J., Shou,J., Sondiky, Shou,J., Shou,J., Sondiky, Shou,J., Shou,J.
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Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, David, L., David, C., Davy-Carroll, L., Dederich, D.A., David, M.S., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Roha, S., Durbin, K.J., David, M.J., David,
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L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, R., Ch
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Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 112720 bases at least 040 Consensus quality: 116666 bases at least 030 Consensus quality: 119165 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
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Center code: BCM
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TITLE JOURNAL REFERENCE

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* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 32 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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TITLE
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Best Local Similarity
Matches 548; Conserv
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           TTTGGACTCTTTCAAGTTCACTGAGGGGCC
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                                                         TCCCTTCGGATCCGCACCCTCCCCTGGGCTCATCTTAAGGCTGCCCCCTTCCTAACCTAC
                                                                                          CTCGGGCCCCAGCTCCGCCTCTGCCAGGTGTCTGGGCTGTTGGCCCCTGCGGCCCAGGGTCC
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                                              TCCCTGCGGATCCGCACCCTCCCCTGGGCCCATCTCAAGGCTGCCCCCCTTCCTCACCTAC
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synthetic construct
artificial sequences.
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Tweak receptor
patent: WO 0145730-A 1 28-JUN-2001;
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/protein_id="CAC50004.1"
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RINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEE
FSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH"
a 266 c 267 g 178 t
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/db_xref="taxon:32630"
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Matches 685
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                                                                                                                                                                                                                                                                                                                                                                                             CDS
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                          298
                       AGCAGGTGTGGATGGGACAGTGAGTGGCTGGGAAGAGCCAAAATCAACAGCTCCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: nisc_mgc@nhgri.nih.góv
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi.R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be fo through the I.M.A.G.E. Consortlum/LIML at: http://image.llnl.gov Series: IRAL Plate: 30 Row: p Column: 5
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 450759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Tissue Procurement: Louis Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: National Institutes of Health In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing Center (NISC), Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg, R.
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Mammalia, Eutheria,
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BC019047.1 GI:17512138
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                                                                                       Similarity
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                                                                                                                                                                          superfamily, member 12"
/protein_id="AAH19047.1"
/db_xref="GI:17512139"
/translation="MAARRSQRRRGERGEPGTALLYPLALGLGLALACLGLLLAVVSLGSRASLSAGEPAQEEVAREDEDDSELMPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAHYEVHPRPGQDGAQADGGYTTCLRP"

1 517 c 481 q 300 +
                                                                                                                                                                                                                                                                                                                                                                                          /note-"Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="MGC:20669 IMAGE:4766071"
/tlssue_type="Primary B-Cells from /clone_lib="NIH_MGC_48"
/lab_host="DH10B-R"_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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Similar to tumor necrosis
member 12, clone MGC:20669
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                                                                    0;
                                                               Score 409.4; DB 9;
Pred. No. 6.1e-97;
0; Mismatches 171;
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                                                                                                                                                                                                                                               --TCCCTGTGGATTTTGAAA--AGATACTATTTTTATTATTATTATTGTGACAAAATGT---T
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          AC127470
AC127470.1 GI:21886866
HTG; HTGS_PHASE1; HTGS_C
                                                                    Pan troglodytes clone unordered pieces.
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El 1 (bases 1 to 215795)

Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Benoks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J.,
Haghighi,P., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Laric,P.,
Haghighi,P., Hansen,N., Ho,S.-L., Maduro,V.B.,
Margulies,E.H., Masiello,C., Maskeri,B., Mastrian,S.D.,
McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R.,
Portnoy,M.E., Prasad,A., Schueler,M.G., Stantripop,S., Thomas,J.W.,
Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (17-UUL-2002) NIH Intramural Sequencing
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Green, E.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number be preserved.
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Sequencing vector: plasmid; n/a; 100% of reads
Sequencing vector: plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 203929 bases at least Q40
Consensus quality: 205865 bases at least Q30
Consensus quality: 209181 bases at least Q20
Insert size: 190000; agarose fp
Insert size: 214395; sum-of-contigs
Quality coverage: 7.30x in Q20 bases; agarose-fp
Quality coverage: 6.47x in Q20 bases; sum-of-contig
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Center clone name: 145D13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: NIH Intramural Sequencing Center Center code: NISC
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89522: contig
89522: gap of u
105537: gap of u
105637: gap of u
121197: contig
121297: gap of u
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                                                                                                          TTCCAGGTTCACTGAGGGGCCCTGGTCTCCCCGCAGTCGTCCCAGGCTGCCGGCTCC---
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                                                                           AGCATCACCACACCTCCCTACCCCACCCCCACTCCACCCCCTC-GCTGCTCCTTGGT
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39313. .49342
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                                                                                                                                                                                                                                                                                                                                                                                                                   Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., NcKernan, K., McLaughlin, J., Weldrim, J., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Vassiliev, H., Vo, A., Wheele
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                                                                           Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Bloom,T., Boyuslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choppel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.
                                                                                                                                                                                                                             Direct Submission
Submitted (08-DEC-1999) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 177703)
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Birren, B., Nusbaum, C.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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       Hagos, B.,
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COMMENT
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                              42862
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------ Project Information
Center project name: L3849
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169559 177703: contig of 8145
Location/Qualifiers
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/db_xref="taxon:9606"
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    Genome Center

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71.0%;
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Pred. No. 8.7e-69;
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Walker, M.A.,

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RESULT 1:
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ORGANISM
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          Akhter.N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J.,
Haghighi,P., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Laric,P.,
Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
Margulies,E.H., Masiello,C., Maskeri,B., Mastrian,S.D.,
McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R.,
McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R.
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HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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    Portnoy, M.E., Prasad, A.,
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    Schueler, M.G.,
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Stantripop, S.,
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unordered
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Submitted (10-JUL-2002) NIH Intramural Sequencing Center,
Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A. Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number be preserved.
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111429
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Center clone name: 045D24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
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vector_side:left*
5942. .8435
                                                                                                                                                            /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="RP42-45D24"
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                                                            /note="assembly_fragment
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                                                                                           TGG-----GTCCTCCATACCCCCTCTTCAGCCACTAAGAGGGGCCGGATGCCAGAGAGAC
                                                                                                                                                                                                                         AGCTCTTCCCACCTCCAGCTCTCC--ACCTCACTAGCTCCCCAGCCCCATTTATCTCCTG
                                                                                                                                                                                                                                                                                                                                                     CCGCTCTCTGAGCACCCCTGTCCCCCTCTGCCCCACCCTGAGCTGCTCCTCCCCCAGACCT 27537
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GGA----TCCCTGTGGATTTTGAAA--AGATACTATTTTTATTATTATTATTGTGACAAAATG
                                AGGGACTAGGCCAGGAGTTCCCCAATGTGAGGGGTCAGAGACCAGGACAGGCTCCTCCCC
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                                                                                                                                                         ACTCCCCAACCCTGGCTGCAGCCCCCCAGGACACTGTGTTGACTGTACTCTGGGTGATGA 27715
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111529. .153553
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73870. .90859
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56691, .73769
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15900. .25224
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Pred. No. 5e-62;
0; Mismatches 243;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Haghighl, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. NISC Comparative Sequencing Initiative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (08-AUG-2002) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence
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AC130192.1 GI:22138443
HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: dbg
Center clone name: 436K21
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Blg Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 164120 bases at least 040
Consensus quality: 168085 bases at least 030
Consensus quality: 170767 bases at least 020
Consensus quality: 170767 bases at least 020
Consensus quality: 170655; sum-of-contigs
Quality coverage: 4.78x in 020 bases; agarose-fp
Quality coverage: 4.57x in 020 bases; sum-of-contig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 177555)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
     3461
3561
6870
6970
13466
13566
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3460: contig of 3460 bp in length 3560: gap of unknown length 6869: contig of 3309 bp in length 6969: gap of unknown length 13465: contig of 6496 bp in length 13565: gap of unknown length 21301: contig of 7736 bp in length
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ORIGIN
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Query Match 20.3
Best Local Similarity 63.8
Matches 487; Conservative
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                                                                                                                                                                                                                                                                                                                      415 CCTGTACTGTCAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGAACTTGCT 474
                 655
                                                         CTTTGGACTCTTCAAGTTCACTGAGGGGCCTTGCTCCCCAGATTCCTTAAACTTTCCC 714
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Note="assembly_fragment"
76771. .115165
/note="assembly_fragment"
115266. .177555
/note="assembly_fragment
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/note="assembly_fragment"
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58825. .76670
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45155 .58724
/note="assembly_fragment
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33820. .45054
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1. .177555
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3561. .6869
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/note="assembly_fragment"
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1. .3460
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/db_xref="taxon:9823"
/clone="RP44-436K21"
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33719: contig of 12318 bp in length
33819: gap of unknown length
45054: contig of 11235 bp in length
45154: gap of unknown length
58724: contig of 13570 bp in length
58824: gap of unknown length
76670: contig of 17846 bp in length
770: gap of unknown length
115165: contig of 38395 bp in length
115265: gap of unknown length
117555: contig of 62290 bp in length
177555: contig of 62290 bp in length
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                                                                                                                                                                                                                                                                                                                                                              Score 237.4; DB 2; Length 177555;
Pred. No. 3e-51;
0; Mismatches 216; Indels 60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             927 others
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	COMMENT	r s	TITLE JOURNAL REFERENCE		AUTHORS	ORGANISM		RESULT 15 AC126925/c LOCUS DEFINITION	Qy 1128 GTT- Db 113571 GTTG	Qy 1074 TG Db 113631 CT	Qy 1014 CT Db 113691 CC	Qy 955 TT Db 113751 CA	Qy 895 AG Db 113811 GG	Qy 835 TC Db 113846 AC	Qy 775 CT Db 113906 TA
code: NISC e: http://www.nisc.nih.gov - http://www.nisc.nih.gov - project name: cwp clone name: 332E11 - Summary Statistics ing vector: plasmid: n/a; 1008 ry: Dye-terminator Big Dye; 100 ry: Dye-terminator Big Dye; 100 y program: phrap; version 0.99 us quality: 148712 bases at le us quality: 151471 bases at le	r: NIH Intramural Sequencing (ion JUL-200 le, Gai	to 161428)	., Legaspi, R., Maduro,Q.L., Maduro,V.B., H., Masiello,C., Maskeri,B., Mastrian,S.D., C., McDowell,J., Paquirigan,C., Pearson,R., Prasad,A., Schueler,M.G., Stantripop,S., Thomas, Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wiggins,L., Young,A., Zhang,LH. and Green,E.D.	strom-Sternberg,S.M. S., Breen,K., Brinkl an,X., Gupta,J.,	Canis familiaris Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	GI PHAS	AC126925 AC126925 AC126925 Canis familiaris clone RP81-332E11, WORKING DRAFT SEQUENCE, 15	GTTAAATGGATATTAAAGAAATAAATCATGATTCTCTT 1167 	TGGATCCCTGTGGATTTTGAAAAGATACTATTTTTATTATTGTGACAAAAT 1127 	CTGGGACTAGGCCAGAAGTTCCCAACTGTGAGGGGGAAAAGCTGGGGACAAGCTCCC 1073 	TTGACTTTGTGCACCAGGCACTGAGATGGGCTGGACCTGGTGGCAGGAAGCCAG-AGAAC 1013	AGCTCCCAAAGCCCCTACTTATCCCTGACTCCCCACCCAC	TCCACAGAGGTATCCTTGCTCTTAACATCCCATCCCACCACACTATCCACCTCACT 894	CTCCTTGGTCCAGTCCTGTCTCCTCAAAGGCAGCCAGAGCTTGTTCACATGTTTCCAT 834

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FEATURES
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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49783: contig of 8902 bp
49883: gap of unknown leading of 9267 bp
59150: contig of 9267 bp
59250: gap of unknown leading of 9292 bp
68779: gap of unknown leading of 10205 bp
68779: gap of unknown leading of 14362 bp
79084: gap of unknown leading of 14362 bp
79084: gap of unknown leading of 14362 bp
102175: contig of 8629 bp
102175: gap of unknown leading of 129410 bp
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                                                                       CCTGTGGATTTTTAAAACAGATATTATTTTTTTTATTATTGTGACAAGATGTCAATAAGT
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Gapop 60.0 , Gapext 60.0
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573.381 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match Length DB	ength		ID	Description
۳	284	100.0	284	19	AAW47525	Homo sapiens tumou
2	249	87.7	249	20	AAY09369	Human tumour necro
ω	249	87.7	249	21	AAB07526	Amino acid sequenc
4	249	87.7	249	21	AAY95338	Human PRO207 antit
5	249	87.7	249	23	AAU86129	Human PRO207 polyp
6	241	84.9	249	19	AAW29745	TNF related endoth
7	241	84.9	249	22	AAE00891	Human TREPA (TNF r
8	207	72.9	273	22	AAU03499	TWEAK extracellula
9	146	51.4	146	22	AAE00895	Human TREPA (TNF r
10	143	50.4	189	19	AAW29746	TNF related endoth

66666655555555555444444444333333332222222111 66366666554321008765432100876543210	111 112 113 114 116
777777770000000000000000000000000000000	143 107 46 32 32 32
$ \begin{array}{c} NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN$	
7449 7449 555 555 555 555 555 555 555 555 555	189 208 211 225 225 58
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AAGU12bb AAN14906 ABB73512 AABB73518 ABB42637 ABB25983 ABB25983 ABB25983 ABB25983 AAM76342 AAM76342 AAM20858 AAM364984 AAM77706 AAB26890 AAM77706 AAM7706 AAM77706 AAM77706 AAM7706	ממות בתות בתות באו
Human secreted pro Extended amino aci M vaccae GVS-9 pro Propionibacterium Peptide #10143 enc Protein #7982 enco Human brain express Human bone marrow Peptide #10488 enc Human bone marrow Peptide #11487 enc Protein #8889 enco Peptide #11950 enc Protein #8889 enco Peptide #11950 enc Protein #889 enco Peptide #11950 enc Propionibacterium Novel human diagno Propionibacterium Novel human diagno Prosophila melanog Streptococcus poly Human EST encoded Human ovarian anti Novel human diagno	n UL4flag TRE n TNRL3 prote e TNRL3 prote musculus tumo o acid sequen n secreted pr

ALIGNMENTS

KW	ΧX	X	×	DE	XX	DΤ	×	AC	×	ID	AAW.	RES
graft rejection.	cancer; autoimmune disease;	TRELL; tumour necrosis fact		Homo sapiens tumour necrosi:		21-JUL-1998 (first entry)		AAW47525;		AAW47525 standard; Protein;	AAW47525	RESULT 1

284

ΑA

Homo sapiens tumour necrosis factor related ligand (TRELL). 21-JUL-1998 (first entry)

TRELL; tumour necrosis factor related ligand; tnf; treatment; cancer; autoimmune disease; immune system; stimulation; suppression; graft rejection.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         characteristics is that Or human tembors record territion (TRELL). TRELL or active fragments can be included with a carrier in pharmaceutical compositions to treat cancer, autoimmune control diseases or immune responses to tissue grafts, or to stimulate or suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening compositions for binding with a detectable label and screening compositions for binding. Algents interfering with TRELL-receptor thinding can also be screened for, can then be administered, optionally with interferon-gamma, to induce cell death or treat, suppress or alter immune responses (especially involving human cadenocarcinoma cells) involving a signal pathway between TRELL and its adenocarcinoma cells) involving a signal pathway between TRELL and its receptor. It's coding sequence can be used in gene therapy for TRELL-related disorders in mammals (especially humans), e.g. tumours, autoimmune and inflammatory diseases or inherited genetic disorders, by introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL.

It may also be of use in the preparation of prepare probes for anticance therapy.
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Best Local S
Matches 284
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07-AUG-1996;
18-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour necrosis factor related ligand - useful for, e.g. treating cancer, auto-immune disease and immune responses to tissue grafts {\sf cancer}
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N-PSDB; AAV18600.
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                         YNRQIGEFIVTRAGLYYLYCQVHFDEGKAYYLKLDLLVDGVLALRCLEEFSATAASSLGP
                                                                                                                                                                          NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR
                                                                                                                                                                                                                                                                                         MSLLDFEISARRLPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLA
                                                                                                                                                                                                                                                                                                      MSLLDFEISARRLPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLA
                                                                                          YNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP
                                                                                                                                                           NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR
                                                                                                                                                                                                                         LGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL
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96US-0023541.
96US-0028515.
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Pred. No. 2.2e-252;
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RESULT 2
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Best Local Similarity
Matches 249; Conserv
                                                                                                                                                                                                                                                             The present sequence represents a human tumour necrosis factor (TNF) and lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has cytostatic activity. Apo-3 ligand can be used to induce apoptosis in mammalian cancer cells, to induce NF-kappaB-dependent transcription to induce JNK/SAPK-dependent responses in mammalian cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; tumour necrosis factor; Apo-3 ligand; lymphotoxin; apoptosis; NF-kappaB-dependent transcription; JNK/SAPK-dependent response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY09369 standard; Protein;
                                                                                                                                                                                                                                                                                                                                           New human Apo-3 ligand (a tumour necrosis factor) homologue
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N-PSDB; AAX56000.
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10-OCT-1997;
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241
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                                                                            MAARRSQRRRGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL
                                      LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL
                                                  LLVDGYLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL
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Conservative (
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97US-0062037
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Pred. No. 2.7e-220;
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AAB07526 standard; protein; 249

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RESULT 4
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a TWEAK protein. The specification describes a method for preventing or treating an immunological disorder and/or inhibiting an immune response in an animal. The method comprises administering a TWEAK blocking agent. The method may be used for preventing and treating immune disorders associated with inappropriate expression and/or activity of TWEAK. These disorders include autoimmune diseases, acute and chronic inflammation, organ transplant rejection, Graft-versus-Host disease (GVHD), lymphoid cell malignancies, septic and other forms of shock, loss of immune responsiveness (as seen in human immunodeficiency virus (HTV) infections) and failure of the immune response to tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Preventing and treating immune responses using modulators, especially antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, useful for treating e.g. inflammation and graft versus host disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TWEAK protein; immunological disorder; immune response; inflammation; TWEAK blocking agent; autoimmune disease; organ transplant rejection; Graft-versus-Host disease; GVHD; lymphoid cell malignancy; shock; tum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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                                                                                                             VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD
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249; Conserv
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Pred. No. 2.7e-220; ...
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21-APR-1999;
28-APR-1999;
14-MAY-1999;
20-JUL-1999;
26-JUL-1999;
15-SEP-1999;
       Novel composition to inhibit neoplastic cell growth or for treating tumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219, PRO221, PRO224, PRO308, PRO301, PRO526, PRO362, PRO356, PRO509 or
                                                                   Ashkenazi I
Napier MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRO207; human; antitumour; tumour; therapy; cytostatic; breast cancer; ovarian cancer; renal cancer; colorectal uterine cancer; prostate cancer; lung cancer; bladder cocentral nervous system cancer; melanoma; leukaemia; neo
                                                                                                                                                                        22-DEC-1998;
08-MAR-1999;
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                                          2000-442668/38.
)B; AAA49717.
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                                                            ı AJ,
Pitti
                                                                                            GENENTECH INC.
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                                                                  Goddard
tti RM,
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99US-0130232
99US-0131445
99US-0134287
99US-0144758
99US-0144598
99WO-US21090
99WO-US21547
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97..10
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128..134
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45..51
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41..249
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24..35
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10..14
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139..1
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36..42
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29..35
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27..33
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                                                                   Godowski PJ,
d WI;
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                                                                           Gurney AL,
                                                                           Marsters
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RESULT 5
AAU86129
IID AAU86129
IID AAU86129
AC AAU8
AC AAU8
AC Huma
XX Huma
DE Huma
XX Huma
KW 1nfi
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Best Local S
Matches 249
08-MAR-1999;
11-MAR-1999;
11-MAY-1999;
02-JUN-1999;
22-JUN-1999;
22-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; neuroprotective.
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leukaemia; neuronal disorder; stromal disorder; blastocoelic diso
inflammatory disorder; immune disorder; angiogenic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
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99WO-US05028.
99US-123972P.
99US-133459P.
99WO-US12252.
99US-140650P.
99US-140653P.
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2.7e-220;
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27-OCT-1998

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standard;

Protein;

AAW29745;

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RESULT 6
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Matches 249;
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26-JUL-1999
28-JUL-1999
17-AUG-1999
11-AUG-1999
01-SEP-1999
15-SEP-1999
15-DEC-1999
01-DEC-1999
01-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAUB6128-AAUB6162 represent the human PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                               TYFGLFQVH
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DB; ABK40255.
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99US-14598P
99US-14622P
99US-149395P
99US-11689P
99WO-US20111
99WO-US20111
99WO-US28313
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99WO-US28314
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llarity 100.0%;
Conservative
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                                                                                                                                      284
                                                                                                                                                                                                                                                                                                                                                                                                              invention.
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1 RM, Roy MA,
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Pred. No. 2.7e-220;
0; Mismatches 0;
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Smith
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RESULT 7
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                                                                                                                                                                                                                                                                                                      The TNF-related endothelium proliferative agent (TREPA), or its activators or agonists, are used to treat a deficit of TREPA, e.g. to CC promote wound healing or tissue graftling, by promoting vascularisation, CC also to induce apoptosis for treating cancer and eliminating autoreactive TreEPA peptides can also be used to target cytotoxic agents or for CC affinity isolation of the corresponding receptor, the nucleic acid for CC which can be used to transform tumour cells to render them more CC responsive to TREPA and to screen for TREPA mimics.

CC Ribozymes, antisense RNA, antibodies or peptides, are used to treat CC responsive to TREPA amount or a wide range of autoimmune conditions, inflammation or a wide range of autoimmune conditions, CC conditions involving abnormal stimulation of epithelial cells (e.g. conditions involving abnormal stimulation of epithelial cells (e.g. cc. conditions) or other angiogenic conditions (e.g. ulcers).
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Best Local
                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detecting nucleic acid encoding TREPA - useful for diagnosis treatment of autoimmune disease, tumours and inflammation
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12-FEB-1997;
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DB; AAV47613.
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                                                                                  sapiens
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                                          249
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                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                      249
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97US-0798692.
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vascularisation; apoptosis; autoimmune; birth control
                                                                                                                                                                                                                                                                     84.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142pp; English.
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                                                                                                                                                                                                                                                                    Score 241; DB 19; Pred. No. 6.1e-213;
                                                                                                                                                                                                                                                           Mismatches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wiley
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10-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inducing angiogenesis in mammal at desired sites for promoting wound healing, by administering soluble fragment of extracellular domain o tumor necrosis factor related endothelium proliferative agent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         grafting; vulnerary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TREPA; TNF related endothelium
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 284
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                                                                        LRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQV
                                                                                                                                       SELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001-280760/29.
DB; AAD04350.
                         LRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQV
                                                                                                                          SELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TREPA (TNF related endothelium proliferative agent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour necrosis factor;
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                                                                                                                                                                                                                                                                              249 AA;
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ilarity 100.0%;
Conservative
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98US-0021706
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/label= Extracellul
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                                                                                                                                                                                                                                        Score 241;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TNF; angiogenesis; wound healing;
proliferative agent; tumour; meta
                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                     6.1e-213;
                                                                                                                                                                                                                                                    ВВ
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RESULT 8
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                                                                                                                                                                                                                                 growth hormone leader, a leucine zipper multimerisation domain, and the extracellular domain of human TWEAK. The fusion protein was used in the isolation of human TWEAK receptor (TWEAKR)-expressing clones from a COS cell human cDNA library. The TWEAK protein is a member of the tumour necrosis factor (TNF) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular disorders retinopathy and the content of the content of
                                          neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, uveitis, macular degeneration and rotroneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and metastatic conditions such as sarcomas and carcinomas, benign tumours and preneoplastic conditions, myocardial angiogenesis, haemophilic joints, scleroderma, vascular adhesions, atherosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preneoplastic condition; myocardial angiogenesis; wound granulation; scleroderma; vascular adhesion; telangiectasia; ischaemia; human; atherosclerotic plaque neovascularisation; coronary atherosclerosis; peripheral atherosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAKR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        retinoblastoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; corneal graft possions.
                      plaque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents a a fusion protein encoded by the expression vector pDC409-LZ-TWEAK. The fusion protein comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modulating angiogenesis in a mammal for treating diseases mediated by angiogenesis, e.g. solid tumours and vascular deficiencies of cardiac peripheral tissue, by administering antagonist or agonist of TWEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-417975/44.
N-PSDB; AAS03964.
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10-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                corneal graft neovascularisation; psoriasis; metastatic condition; mallgnant tumour; sarcoma; carcinoma; benign tumour; haemophilic joint;
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                      telangiectasia, wound
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Best Local
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                               The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNP) family molecules designated as TREPA (TNF related endothelium proliferative agent). Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis in human for promoting wound healing and for vascularising grafted tissue for successful grafting and to promote tissue grafts.
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10-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           grafting; vulnerary.
                                                                                                                            Example
                                                                                                                                                               tumor necrosis factor related
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980S-0021706
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                     to promote tissue grafts.
human TREPA fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                              proliferative agent protein
                                                                                                                                                                                                                                                                                                                                                                                                                       agent; tumour; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 273;
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Sequence

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RESULT 10
AAW29746
ID AAW29746
XX AAW29746
AC AAW29
AC AA
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                                                                                                                                              CC The TNF-related endothelium proliferative agent (TREPA), or its CC activators or agonists, are used to treat a deficit of TREPA, e.g. to CC promote wound healing or tissue grafting, by promoting vascularisation, CC also to induce apoptosis for treating cancer and eliminating autoreactive TrepA peptides can also be used to target cytotoxic agents or for CC affinity isolation of the corresponding receptor, the nucleic acid for CC which can be used to transform tumour cells to render them more CC responsive to TREPA and to screen for TREPA mimics. CC Ribzymes, antisense RNA, antibodies or peptides, are used to treat CC TREPA-associated diseases, e.g. tumours and metastases (by inhibiting CC conditions involving abnormal stimulation of epithelial cells (e.g. catherosclerosis), for birth control (inhibiting ovulation and placental CC formation) or other angiogenic conditions (e.g. ulcers).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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  Query Match
Best Local S
Matches 143
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detecting nucleic acid encoding TREPA - useful for diagnosis treatment of autoimmune disease, tumours and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wiley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 16; Page 125-6; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9835061-A2
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                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ABBO ) ABBOTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-FEB-1998;
12-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens
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                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0021706.
97US-0798692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US02859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferative agent; TREPA;
vascularisation; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.4%;
100.0%;
                          100.
                             .0%;
Score 143; DB
; Pred. No. 4.6
0; Mismatches
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Pred. No. 6.4e-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agent protein
                          , DB 19
                          19;
e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wound healing; cancer; autoimmune; birth cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126;
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                                                   Length 189;
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Conservative

0,

Indels

0,

Gaps

0;

밁 Q

47

Matches 1 Query Match Best Local

al Similarity 143; Conser

50.4%; llarity 100.0%; Conservative

0

Score 143; DB 22; Pred. No. 4.6e-123; 0; Mismatches 0;

Length 189;

0;

Gaps

0

142

IAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQ 201

IAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQ

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RESULT 11
AABOO892
ID AABOO892
XX AABOO
XX AABOO
XX DE Human
XX Human
XX Human
XX US632
XX US632
XX US632
XX 12-FF
PR 10-FF
PR 10
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                                                      The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molecules designated as TREPA (TNF related endothelium proliferative agent). Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis in human for promoting wound healing and for vascularising grafted tissue for successful grafting and to promote tissue grafts. The present amino acid sequence is human UL4flag TREPA soluble construct. This sequence which is a biologically active molecule is capable of inducing proliferation in HUVEC (human umbilical vein endothelial cells) cells.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; tumour necrosis factor; TNF; angiogenesis; wound healing; TREPA; TNF related endothelium proliferative agent; metastasis; vulnerary; HUVEC; human umbilical vein endothelial cell; UL4flag
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                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Column 75-78; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inducing angiogenesis in mammal at desired sites for promoting wound healing, by administering soluble fragment of extracellular domain o tumor necrosis factor related endothelium proliferative agent protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wiley
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10-FEB-1998;
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      189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TREPA soluble
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98US-0021706
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RESULT 12
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                                             This invention describes isolated Tumor Necrosis Factor (TNF) family C receptor polypeptides: APO4, APO6, APO8 and APO9 or their active CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic comolety. APO4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding of CC agents to the polypeptide/active fragment which is extracellular, or cexpressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/active fragments are also useful for screening CC for agonists and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or creatment of disease are also identified using APO4 polypeptides/active fragments are specifically interact components and APO4 signal transducer molecules that specifically interact cuseful for diagnosis/treatment of developmental or gestational contents are also activity. The method is performed in vivo or in vitro. APO polypeptides are also indunogens for preparing antibodies. APO4 is also useful for diagnosis/treatment of developmental or gestational contents. APO8 was transfected to human breast carcinoma cell line
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 40; Fig 13A; 156pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Tumor Necrosis Factor family receptor polypeptides and ligands - useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
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N-PSDB; AAX23424.
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This invention describes isolated Tumor Necrosis Factor (TNF) family receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer by determining levels of APO4 is useful for diagnosing prostate cancer by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic moiety. APO4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding of agents to the polypeptide/active fragment which is extracellular, or expressed on the cell surface. The binding is preferably performed in vivo. APO4 polypeptides/active fragments are also useful for screening for agonists and antagonists by binding and observing the changer in APO4 active, Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              developmental abnormality; gestational abnormalitity; prostate cancer; APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disea cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
                                                                                                                                                                                                                                                    Claim 40;
                                                                                                                                                                                                                                                                               New Tumor Necrosis Factor family receptor polypeptides useful for diagnosis and treatment of prostate cancer \epsilon developmental or gestational abnormalities
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DB; AAX23425.
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                                                                                                                                                                                                                                                  Fig 13B;
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                      The sequence is that of mouse tumour necrosis factor related ligand (TRELL). TRELL or active fragments can be included with a carrier in pharmaceutical compositions to treat cancer, autoimmur diseases or immune responses to tissue grafts, or to stimulate or suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for, can then be administered, optionally with interferon-gamma, to induce cell death or treat, suppress or alter immune responses (especially involving)
                                                                                                                                                                                                                                                                                                                                                                                 Tumour necrosis factor related ligand - useful for, cancer, auto-immune disease and immune responses to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRELL; tumour necrosis factor related ligand; tnf; treatment;
cancer; autoimmune disease; immune system; stimulation; suppression;
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                                                                                                                                                                                                                                                                                                                               Claim 12;
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07-AUG-1996;
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                                                                                                                                                                                                                                                                                                                         Pages 48-50; 69pp; English.
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  involving
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No.
ma, to induce cell death or
responses (especially involving hum
a signal pathway between TRELL and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20; I
6.1e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                    tissue
                                                                                                                                                                                                                                                                                                                                                                         .g. treating
issue grafts
                                                                                                                                                                                                                  autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                              human
  its
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RESULT 15
AAB07527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                       The present sequence represents a TWEAK protein. The specification describes a method for preventing or treating an immunological disorder and/or inhibiting an immune response in an animal. The method comprises administering a TWEAK blocking agent. The method may be used for preventing and treating immune disorders associated with inappropriate expression and/or activity of TWEAK. These disorders include autoimmune diseases, acute and chronic inflammation, organ transplant rejection, Graft-versus-Host disease (GVHD), lymphoid cell malignancies, septic and other forms of shock, loss of immune
                                                                                                                                                                                                                                                Preventing and treating immune responses using modulators, especially antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, useful for treating e.g. inflammation and graft versus host disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWEAK protein; immunological disorder; immunety autoimmune disease; Graft-versus-Host disease; GVHD; lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor. It's coding sequence can be used in gene therapy for TRELL-related disorders in mammals (especially humans), e.g. tumours, autolimmune and inflammatory diseases or inherited genetic disorders, by introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL. It may also be of use in the preparation of prepare probes for screening natural/synthetic DNAs for TRELL-encoding sequences
                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB07527;
                                                                                                                                                                                                                                                                                                                 WPI; 2000-476036/41
                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JAN-2000; 2000WO-US01044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB07527 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                             intections)
                                            responsiveness
                                                                                                                                                                                                                                                                                                                                                                           (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                             15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a soluble recombinant murine TWEAK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEE 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . Similarity
32; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense
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                             ess (as seen in and failure of
                                                                                                                                                                                                                    Fig 1; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                             99US-0116168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.3%;
                           human immunodeficiency virus (HIV) the immune response to tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.7e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organ transplant cell malignancy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rejection;
shock; tum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Matches Query Match Best Local

Similarity 32; Conserv

Conservative

0;

11.3%; 100.0%;

Score 32; DB Pred. No. 4.7 0; Mismatches

DB 21; 4.7e-21

Length 225

Indels

0;

Gaps

0

Sequence

225

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RESULT 17
AAG01266
ID AAG01
XX
AC AAG01
XX
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AAG01265
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                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                     Matches
                                                                                                                                                                                                                                    The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained; the full 5' may be a sequenced to obtain full length cDNAs and genomic cDNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to detain average to make the content.
                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
             AAG01266;
                                      AAG01266 standard;
                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; SEQ ID 5346; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAC01271.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas Milne Edwards J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-OCT-2000
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                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                               regulatory sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46
                                                                                                                1 MSLLDFEIS
                                                                                                    MSLLDFEIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5' EST;
                                                                                                                                                   Similarity
9; Conserv
                                                                                                                                                                                                       58
                                                                                                                                                                                                                               sequences
                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome mapping.
                                                                                                    54
                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                    Protein;
                                                                                                                                                             3.2%;
100.0%;
                                                                                                                                                                                                                               and to design expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58
                                      58
                                                                                                                                                     0;
                                                                                                                                                                Score 9; 1
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO: 5346.
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                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tag; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111
                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                               and secretion vectors.
                                                                                                                                                     0
                                                                                                                                                                           Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                              tag (5' EST) for to 5'ESTs and for
                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA isolation
                                                                                                                                                     0;
                                                                                                                                                     Gaps
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RESULT 18
AAY14906
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                                                                                                                                                                                                                                                                                                                                      Q.
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Best Local Similarity
""" (hes 9; Conserva
The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted
                                                                                                                                                                                                                                AAY14906 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; SEQ ID 5347; 71pp + CD-ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-OCT-2000
                                                       Mycobacterium vaccae protein; antigen; T cell activation; cytokine; dendritic cell maturation; infectious disease; immune disorder; car dendritic cell maturation; infectious disease; immune desorder; car respiratory system; mycobacterial infection; allergy; tuberculosis; leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis
                                                                                                                                                                                                  AAY14906;
                           squamous
                                            leprosy; sarcoidosis;
dermatitis; eczema; a
                                                                                                                                   Extended amino acid sequence
                                                                                                                                                                   25-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                                                                                                                                                                          46 MSLLDFEIS 54
                                                                                                                                                                                                                                                                                                                                         1 MSLLDFEIS 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000-500381/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC01272
                                                                                                                                                                                                                                                                                                                                                                                                                                58
                                              eczema; alopecia areata; skin
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; expressed sequence
chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein, SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9905-0122487
                                                                                                                                                                                                                              protein;
                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                    3.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duclert A,
                               melanoma
                                                                                                                                                                                                                                                                                                                                                                                    Score 9; ; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                     for GVs-9.
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
                                               cancer;
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mapping procedures
                                               basal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                            cancer;
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Mycobacterium

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RESULT 19
ABB73512
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                                                                                                                                                                                                                                                                                                                                           M. vaccae proteins. The M. vaccae proteins may be employed to activate T cells and natural killer cells, to stimulate the production of cytokines, to enhance the expression of co-stimulatory molecules on dendritic cells and monocytes, and to enhance dendritic cell maturation and function. The proteins can be expressed by standard recombinant methodology. Pharmaceutical compositions comprising the proteins or nucleic acid sequences encoding the proteins can be used for the treatment, prevention, and detection of disorders including infectious cisseases, immune disorders and cancer. In particular, the compounds and methods are used for treatment of diseases of the respiratory system, such as mycobacterial infections, asthma, allergies, tuberculosis, leprosy, sarcoidosis and lung cancers, and disorders of the skin such as psoriasis, atopic dermatitis, eczema, allergic contact dermatitis, and protein areata, and skin cancers such as basal carcinoma, squamous cell
                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04 - DEC - 1998;
23 - DEC - 1997;
11 - JUN - 1998;
17 - SEP - 1998;
                                                                        alopecia areata;
antipsoriatic; d
                                                                                                                 M vaccae GVs-9
                                         Mycobacterium
                                                                                            Skin disorder;
                                                                                                                                      08-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 209-210;
                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention provides heat-killed Mycobacterium vaccae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1999
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                                                                                                                                                         ABB73512;
                                                                                                                                                                              ABB73512 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-DEC-1998;
                                                                                                                                                                                                                                282
                                                                                                                                                                                                                                                     60
                                                             immune response;
                                                                                                                                                                                                                                                    ALGLGLALA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-430163/36
                                                                                                                                                                                                                                ALGLGLALA
                                                                                                                                                                                                                                                                         Similarity 9; Conser
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                                                                                                                                                                                                                                                                                                                                     and melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune response
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                                                                                                                                                                                                                                                                                                                  748
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                                                                                                                                    (first entry)
                                          vaccae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0996624.
97US-0997080.
97US-0997362.
98US-0095855.
98US-0156181.
                                                             psoriasis; atopic dermatitis; allergic contact dermatitis; a; skin cancer; Mycobacterium vaccae; melanoma; cytostatic; dermatological; antiinflammatory; antiallergic; ponse; immunomodulatory.
                                                                                                               protein SEQ
                                                                                                                                                                                                                                290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243pp; English.
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                                                                                                                                                                              749
                                                                                                                                                                                                                                                                                 Score 9; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      an antigen
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                                                                                                                154.
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20;
                                                                                                                                                                                                                                                                                            20;
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                                                                                                                                                                                                                                                                                           Length 748;
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AAU51863
δÃ
                                                                                                                                                                                                                                                                                                                                                                  В
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Best Local S
Matches 9
                                                                     21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                              Skeiky YAW,
WPI; 2001-616774/71
                                                                                                                                    01-NOV-2001
                                                                                                                                                        WO200181581-A2
                                                                                                                                                                                                                                                                                            AAU51863;
                                                                                                               20-APR-2001;
                                                                                                                                                                                                 dermatological;
                                                                                                                                                                                                                                                                        27-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watson
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SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
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              Skeiky YAW, Persing
L'maisonneuve J, Zha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes immunogenic protein #12759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU51863 standard; Protein; 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        deglycolipidated culture filtrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method of inhibiting skin inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALGLGLALA 68
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                                                                                                                               CORIXA CORP.
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9; Conserv
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                                                                                                                                                                                           2000US-199047P.
2000US-208841P.
2000US-216747P.
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                                                                                                                                                                                                                                                                                                                                             2001WO-US12865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              osteopathic;
              Zhang
                                                        DH,
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100.0%;
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Mitcham JL, wung
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                                                    Wang SS,
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                      D,
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                                                        Bhatia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteomyelitis;
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RESULT 21
ABB42637
ID ABB42637
XX ABB42637
AC ABB42
XX Pept1
XX Humar
XX Humar
XX Homo
OS Homo
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Best Local S
Matches 8
                                                                                                                                                         21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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Note: The sequence data for this patent did not form part of the printer specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                       30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                          04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide #10143 encoded by human foetal liver single exon probe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
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8; Conserv
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                                                                                                         MOLECULAR DYNAMICS INC
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                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID No 13058;
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                                                                                                                                                      2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234685.
2000US-0236359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                     Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression; single exon nucleic
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Pred. No. 13;
0; Mismatches
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                                                        Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid
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s are used in
s caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probe
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RESULT 22
ABB25983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention.
                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
        The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart ABA21535-ABA41305). The present sequence is a protein encoded by one probe. The probes may be used for predicting, measuring and displaying the probes may be used for predicting.
                                                                                                                                                                                                                                                                                                                                                         Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       analyzing
                                                                Claim
                                                                                                                     WPI;
                                                                                                                                          Penn
                                                                                                                                                                                                                                                                       30-JAN-2001;
                                                                                                                                                                                                                                                                                            09-AUG-2001
                                                                                                                                                                                                                                                                                                                  WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                         23-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB25983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB25983 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single
                                                                                                                                                                                             21-SEP-2000;
27-SEP-2000;
                                                                                                                                                             (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 LGLGLALA 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 LGLGLALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : The sequence data for this patent did not form p
ted specification, but was obtained in electronic
WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                     2001-488899/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                     #7982
                                                                                                                                                               MOLECULAR DYNAMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                         Hanzel
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                                                                                                                                                                                  2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0234683.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                              nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                        2001WO-US00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
                                                                ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                    encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO 35272; 639pp +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression
                                                                                                                                         DK,
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                                                                27753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.8%;
                                                                                                                                          Chen
                                                                                                                                                                                                                                                                                                                                                                                                    probe
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                                                                                                                                          Σ
                                                               530pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon nucleic acid human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 8;
NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence listing;
                                                                                                                                                                                                                                                                                                                                                                                                     measuring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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expression

predicting, measuring and from the human heart via

displaying microarrays.

such

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RESULT 23
AAM63528
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Best L
 Best Local
Matches
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                               Query Match
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                 probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                          Single exon nucleic brains -
                                                                                                                                                                                                                                                                                                                                                         Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; brain expressed exon; genumicroarray; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200157275-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epilepsy; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                    Sequence
                                                                                                                                                                                                     The present invention
                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                        (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAM63528 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
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h 2.8%; Sy Similarity 100.0%; Si
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8; Conserv
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                                                                                                                                                                                                                                      SEQ
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; 2000US-0207456.
; 2000US-0608408.
; 2000US-0632366.
; 2000US-0234687.
; 2000US-0236359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed single exon probe
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                                                                                                                                                                                                                                      ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                        DYNAMICS INC
                                                                                                                                                                                                                                                                                       acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.8%;
                                                                                                                                                                                                     provides a number of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                     Chen
                                                                                                                                                                                                                                  35633; 650pp +
                                                                                                                                                                                                                                                                                     probes
                                                                                                                                                                                                                                                                                                                                                       Σ
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               Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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Pred.
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                                                                                                                                                                                                                                                                                     for analyzing
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   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        multiple sclerosis; probe;
multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . No. I
                                                                                                                                                                                                                                  Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
13;
                   DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoded protein
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                                                                                                                                                                                                                                                                                     gene expression
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 0;
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                               Length 55;
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                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ
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   DX DX AX
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RESULT 24
AAM76342
                                  RESULT 25
AAM20858
                                                                                                                                 Query Match
Best Local S
Matches
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03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                       samples,
                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                  probes which are derived from genomic secured exon bone marrow. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-FEB-2000;
26-MAY-2000;
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone marrow - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microarray;
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AAM20858;
                     AAM20858
                                                                                                                                                                                                                                                bone
                                                                                                                                                                                                                                                                                                Example 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                                           (MOLE-)
                                                                                   12
                                                                                               61 LGLGLALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGLGLALA
                                                                                                                                                                                                          marrow. They can be used to measure gene expression in bone marrow les, which may enable the improved diagnosis and treatment of cances as lymphoma, leukaemia and myeloma. The present sequence is a ein encoded by one of the probes of the invention.
                                                                                   LGLGLALA 19
                                                                                                                                                                                                                                                                                                                                                                                  SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
                                                                                                                                  Similarity
8; Conserv
                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                 Hanzel
                                                                                                                                                                                   55
                                                                                                                                                                                                                                                                                              SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               marrow expressed exon; gene expression analysis;
                                                                                                                                 2.8%;
ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                 2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0180312
2000US-0207456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000US-0608408.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressed
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                       Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    leukaemia; lymphoma; myeloma
                                                                                                                                                                                                                                                                                              36648; 658pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                   Chen
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                                                                                                                                              Score 8;
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                                                                                                                                 ore 8; DB 2;
red. No. 13;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   Rank DR;
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                                                                                                                                                          22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                   0;
                                                                                                                                                          Length
                                                                                                                                                                                                                                                           expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ
                                                                                                                                   Indels
                                                                                                                                                          55
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                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                              English.
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                                                                                                                                   0,
                                                                                                                                   Gaps
                                                                                                                                   0
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Peptide #7292 encoded by probe

for measuring

cervical gene expression.

12-OCT-2001

(first entry)

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RESULT 26
AAM36451
ID AAM36
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                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                        genetic
                                                                                                                               AAM36451 standard;
                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                  analyzing
                                                                                                                                                                                                                                                                                                                                                                                                          Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cervical
                         WO200157272-A2
                                       Homo sapiens
                                                       Probe; microarray;
genetic disorder.
                                                                               Peptide #10488 encoded by probe for measuring placental gene
                                                                                                17-OCT-2001
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W0200157278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probe; human; microarray;
                                                                                                                                                                                                                                                                             cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-2000;
                                                                                                                                                                      12
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                                                                                                                                                                     LGLGLALA 68
                                                                                                                                                                                                                                                                                                                                                                                          2001-488901/53.
                                                                                                                                                                                                                                                                                                                                                                  genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells
                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer
                                                                                                                                                                                                                                                                                                                                                 SEQ ID No 25684; 487pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Hanzel
                                                                                                                                                                                                                                     55
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0233359.
2000GB-0024263.
                                                                                                                                                                                                     Conservative
                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                          DK,
                                                                                                                               Protein;
                                                               human;
                                                                                                                                                                                                            2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene expression; cervical epithelial cell;
                                                               placenta;
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                                                                                                                                                                                                            Score 8
Pred.
                                                                                                                               Ā
                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                              NO.
                                                               antenatal diagnosis;
                                                                                                                                                                                                        DB
13;
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                                                                                                                                                                                                                     Length
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                                                                               expression
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                                                                                                                                                                                                                                                                                                                    SENPS
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                                                                                                                                                                                                                                                            RESULT 27
ABG45635
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Best Local
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                           Sequence
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04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
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21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                         Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disfamilial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                             Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analyzing
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                                                                                                                                        30-JAN-2001;
                                                                                                                                                                               15-NOV-2001
                                                                                                                                                                                                                     WO200186003-A2
                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG45635 standard;
                                                                                                                                                                                                                                                                                               hyaline membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human genetic disorders.
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zing gene expression in human placenta .
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0234687.
2000US-0236359.
2000US-180312P.
2000US-207456P.
2000US-0608408.
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoded by genome-derived single exon probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression in human placenta
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                                                                                                                                                                                                                                                                                                   disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC sample derived from human lung, comprising (a) contexting years of the array with CC a collection of detectably labeled nucleic acids derived from human lung comprising (a) contexting the label detectably bound to each probe of CC (a) algorithmically predicting at least one exon from genomic sequences CC (a) algorithmically predicting at least one exon from genomic sequences CC of the eukaryote; and (b) detecting specific hybridisation of detectably CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, CC having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, CC comprising (a) identifying exons from genomic sequence by the method CC above and (b) measuring the expression of each of the exons in several CC tissues and/or cell types using hybridisation to a single exon CC microarrays having a probe with the exon, where a common pattern of CC expression of the exons in the tissues and/or cell types indicates that CC the exons should be assigned to a single gene; a peptide comprising one CC orders of 12011 sequences, mentioned in the specification, or encoded by the CC expression analysis, and for identifying exons in a gene, particularly cusing human lung derived mRNA and for the study of lung diseases (CC), interstitial lung disease (ILD), familial idiopathic pulmonary CC Nateman-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary CC Nateman-Pick disease, Hermansky-Pudlak syndrome, sarcoidosis, pulmonary can be considered to pulmonary in the componence of the proposition of the expression and considered to a single exon the proposition of the expression and considered to a single exon to a si
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spatially-addressable set of single exon nucleic acid measure gene expression in human lung samples -
                           04-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                         ABB43981;
                                                                                                                     ABB43981 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the printed specification, but format directly from WIPO at
                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                     61 LGLGLALA 68
                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to a spatially-addressable set of single exon leic acid probes for measuring gene expression in a sample derived
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                                                                                                                     Peptide;
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100.0%;
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RESULT 29
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Best Local Similarity
Matches 8; Conserv
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03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fetal liver. The present sequence is a peptide curve. ". - nucleic acid probe of the invention.

Note: The sequence data for this pattent did not form part of printed specification, but was obtained in electronic format from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                          Human; gene expression; heart; microarray; vascular system; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 27;
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26-MAY-2000;
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                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         measuring and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates
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2000US-0207456.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon nucleic acid probes useful for human fetal liver -
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WO200157274-A2

09-AUG-2001

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RESULT 30
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27-SEP-2000;
04-OCT-2000;
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     measuring human gene expression in a sample derived from human heart (see ABA21335 ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fire wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single
hearts
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                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                              microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
                                                                                                                                                                                                                                                                          05-NOV-2001
                                                                                                   30-JAN-2001;
                                                                                                                                                  WO200157275-A2
                                                                                                                                                                                                                         Human; brain expressed exon; gene expression analysis; probe;
                                                                                                                                                                                                                                                 Human brain expressed single
                                                                                                                                                                                                                                                                                                   AAM64984;
                                                                                                                                                                                                                                                                                                                          AAM64984 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 h 2.8%; Score 8; DB Similarity 100.0%; Pred. No. 16 8; Conservative 0; Mismatches
                                                                                                                                                                                                  cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid probes
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0024263.
 2000US-0180312.
2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
2000US-0234263.
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                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                  exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for analyzing gene expression in human
                                                                                                                                                                                                                                                 probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DR
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16;
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Matches
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26 - MAY - 2000;
30 - JUN - 2000;
03 - AUG - 2000;
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1706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Single
The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the hu
                                              Human genome-derived single exon nucleic acid probes useful analyzing gene expression in human bone {\tt marrow} -
                                                                                               Penn
                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                        microarray;
                                                                                                                                                                                                                                                                                                                    Human bone marrow expressed probe encoded protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                          AAM77706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epilepsy and cancers. The present sequence is a protein encoded by one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention
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                           Example 4; SEQ ID NO:
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                  Human;
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                                                                                                                  (MOLE-)
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                                                                                               SG,
                                                                            2001-488900/53.
                                                                                                                                                                                                                                                                                                  bone
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8; Conserv
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                                                                                               Hanzel
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                                                                                                                                                                                                                                                                                          marrow expressed e
cancer; leukaemia;
                                                                                                                                   2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-02346359.
2000US-0236359.
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                                                                                               DK,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37089; 650pp +
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                             38012; 658pp + Sequence Listing;
                                                                                               Chen W,
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Pred. No
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lymphoma;
                                                                                                Rank DR
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16;
                                                                                                                                                                                                                                                                                         expression analysis; myeloma.
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PR 30-JI
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PR 27-SI
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26-MAY-2000;
30-JUN-2000;
                                                                                                                                                                                                                                 The present invention relates to human single exon nucleic acid probes (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded by one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably
                                                                                                                                                                 Note: The sequence data for this patent did not form part of t specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is a protein encoded by one of the probes of the invention.
                                                                                                   Sequence
                                                                                                                                                                                                                   cervical cancer
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27-SEP-2000;
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                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genome-derived single exon nucleic acid probes useful for zing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                                                                                                                                      27; SEQ ID No 26447; 487pp; English.
         Similarity
8; Conserv
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2000US-0207456.
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2000US-0234687.
2000US-0236359.
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           Conservative
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2.8%; 5c.
100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC
    Score 8; DB 2; Pred. No. 16; 0; Mismatches
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Pred. No.
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16;
                              DB 2
                                                    22;
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         0;
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RESULT 34
ABG46737
ID ABG46
XX
AC ABG46
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XX
DE Humar
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AAM37923
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Best Local S
Matches 8
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
Human peptide encoded by genome-derived single exon probe SEQ ID 36402
                                              19-AUG-2002
                                                                                                                                      ABG46737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes (SENP: see ARI31315-AAI57546). The present sequence is a peptide encoded by on such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single analyzing gene expression in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID No 38192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-488897/53.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide #11960 encoded by probe
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                                                                                                                                                                                                                                                                                            61 LGLGLALA
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                                                                                                                                                                                                                                                                                                                                      Similarity
8; Conserv
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                                                                                                                                      standard;
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ilarity 100.0%;
Conservative
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2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
                                              (first entry)
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                                                                                                                                                                                                                                                                                            89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DK,
                                                                                                                                   Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
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human placenta -
                                                                                                                                                                                                                                                                                                                                                        Score 8; I
                                                                                                                                                                                                                                                                                                                                    ore 8; DB 2;
red. No. 16;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rank DR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measuring placental gene expression.
                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probes useful
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                                                        0;
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CC mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising cc (a) algorithmically predicting at least one exon from genomic sequences co of the eukaryote; and (b) detecting specific hybridisation of detectably labeled nucleic acids from eukaryote lung mRNA, to a single exon probe, cc having a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, cc comprising (a) identifying exons from genomic sequence by the method cc above and (b) measuring the expression of each of the exon in several ctissues and/or cell types using hybridisation to a single gene, cc microarrays having a probe with the exon, where a common pattern of cc expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one cf 12011 sequences, mentioned in the specification, or encoded by the cxoression analysis, and for identifying exons in a gene, particularly csing human lung derived mRNA and for the study of lung diseases cc (copp), interstitial lung disease (ILD), familial idiopathic pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes; the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disfamilial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                      pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary dyskinesis, pulmonary hyper
                                                                                                                                                      fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease,
Niemann-Pick disease, Hermansky Pudlak syndrome, sarcoidosis, pulmonary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spatially-addressable set of single exon nucleic acid probes, used measure gene expression in human lung samples - \,
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03-AUG-2000;
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26-MAY-2000;
                                                                                                                            haemosiderosis,
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27-SEP-2000;
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2000US-236359P.
2000GB-0024263.
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2000US-207456P.
2000US-0608408.
2000US-0632366.
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                                                                                                                        pulmonary histiocytosis,
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primary ciliary dyskinesis, pulmonary disease. The present sequence is a non-
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CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC and gene mapping, and in recombinant production of (II). The CC and gene mapping, and in recombinant production of (II). The CC polypucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC imaging of sites expressing (II). (I) and (II) are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CCC and to produce other types of data and products dependent on DNA and CCC diagnostic amino acid sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                           biodiversity
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N-PSDB; AAS67910.
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder.
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RESULT 36
ABG03663
           The invention relates to isolated polynucleotide (I) and CC polyneptide (II) sequences. (I) is useful as hybridisation probes, CC polynerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags (C for identifying expressed genes. (I) is useful in gene therapy techniques (I). (II) is useful for generating antibodies against it, detecting or (II). (II) is useful for generating antibodies against it, detecting or Quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CT he polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human. CC Note: The sequence data for this patent did not appear in the printed constraint of the patent of the printed in all of the printed did not appear in the printed constraints.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n; chromosome mapping; gene mapping; gene therapy; forensic
supplement; medical imaging; diagnostic; genetic disorder
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RESULT 37
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           presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this parent did not form part of the printed not presence.
                                                                                                                                                                    pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
                                                                                                                                                                                                                                                                Sequences AAU39105-AAU68017 represent Propionibacterium acnes polypeptides. The proteins and their associated DNA sequences
                                                                                                                                                                                                                                                                                                            Example 1; SEQ ID No 22477; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes vaccinating against and
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02-JUN-2000; 2000US-208841P
07-JUL-2000; 2000US-216747P
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 obtained
                                                                                                                                                                                                                                                                                                                                                           polypeptides and nucleic acids useful for diagnosing infections, especially useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mitcham JL, Wang
, Jen S, Carter
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in electronic format
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RESULT 38
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                          CC for identifying expressed genes. (1) is useful in gene therapy techniques (2) to restore normal activity of [II] or to treat disease states involving CC (II). (II) is useful for generating annibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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Matches
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                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                   polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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8; Conservative (
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2000US-0649167
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61 LGLGLALA

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RESULT 39
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                                                                                             cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polyncelectides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activino/inhibin activity and may be useful in the diagnosis and/or received.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; cytokine; cell proliferation; cell differentiation; gene vaccine; peptide therapy; stem cell growth factor; haematopoiesi tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human polypeptide SEQ ID NO
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                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 21986; 1399pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                              diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                   Tang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system disorders; arthritis; inflammation
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Sequence
                           at ftp.wipo.int/pub/published_pct_sequences
                                       Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
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18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                       The invention relates to the encoded proteins (AAC
                                                                                                                                                                                                                                                                                            Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-2001; 2001WO-US04927
                                                                       inflammation.
                                                                                    treatment of cancer, leukaemia, nervous system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 LGLGLALA
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nes 8; Conserv
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 117
                                                                                                                                                                                                      on relates to human polynucleotides (AAI79941-AAI93841) and proteins (AAO00010-AAO13910) that exhibit activity elating to
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Conservative (
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                                                                                       arthritis and
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RESULT 40
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid detection reagent for detecting 1000~\rm or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila; developmental biology; cell signalling; insecticide;
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N-PSDB; ABL11815.
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11-JUL-2000; 2000US-0614150.
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                                                                                                                          LLLAVVSL 23
                                                                                                                                                                                                                                                     Similarity 100.8; Conservative
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100.0%; Pred. No. 42;
tive 0; Mismatches
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Result Total number of hits satisfying chosen parameters: Database : Post-processing: Listing first 65 summaries Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Word size : Searched: Scoring table: Title: Perfect score: Run on: OM protein - protein search, using sw model Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Score Query Match Length DB OLIGO Gapop 60.0 , Gapext 60.0 March 31, 2003, 14:07:46; Search time 39 Seconds (without alignments) 700.056 Million cell updates/sec US-09-245-198A-4 284 283224 seqs, 96134422 residues PIR_73:* MSLLDFEISARRLPLPRSLG.... pir1:*
pir2:*
pir3:*
pir4:* GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. Ħ SUMMARIESPWAHLKAAPFLTYFGLFQVH 284 283224

RESULT 2 S78376

photosystem I P700 apoprotein A2 - Odontella sinensis chloroplast

ALIGNMENTS

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R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G. Jung, K.H.; Alam, M.; Freitas, T. Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000 A; Authors: Hou, S.; Danitels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, A; Title: Genome sequence of Halobacterium species NRC-1. A; Reference number: A84160; MUID:20504483; PMID:11016950 A; Accession: G84168
                                                                                                                                                                                                                                                                                                                                                                                         RESULT
G84168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A58208
R;Hunt, J.G.; Kasinsky, H.E.; Elsey, R.M.; Wright, C.L.; Rice, J. Biol. Chem. 271, 23547-23557, 1996
A;Title: Protamines of reptiles.
A;Reference number: A58208; MUID:96394458; PMID:8798564
A;Accession: A58208
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-58 <HUN>
C;Superfamily: sperm histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protamine I-1 - painted turtle
C;Species: Chrysemys picta (painted turtle)
C;Date: 08-Nov-1996 #sequence_revision 08-N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant Mol. Biol. Rep. 13, 336-342, 19
A;Title: The Chloroplast Genome of a
A;Reference number: S78238
                                                                                                                                                                                                                                                                                                   hypothetical protein Vng0080h [imported] - Halobacterium sp. NRC-1 C;Speckes: Halobacterium sp. NRC-1 C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: G84168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; nucleic acid sequence not shown; A;Molecule type: DNA A;Residues: 1-733 <KOW>
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C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 20-Jun-2000
C;Accession: S78376
C;Accession: S78376
R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
                                        A; Cross-references:
                                                                A; Residues:
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, Nove
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Rep. 13, 336-342,
                                                              <ST0>
                                        GB: AE004437;
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-342, 1995
                                     NID:g10579733; PIDN:AAG18715.1; GSPDB:GN00138
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RESULT D83080

hypothetical

protein

PA4521 [imported]

Pseudomonas

aeruginosa

(strain

PAO1)

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R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, ; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; Oroc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular patle A;Reference number: AD3252; PMID:11756688
A;Accession: AG3547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Ju1-2000
C;Accession: E72374
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                 A; Gene: BMEI1U3U4
A; Map position: II
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                                                                                                                                                      A; Experimental source: C; Genetics:
                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-220 < KUR>
                                                                                                                                                                                                                                                                                                                                     bicyclomycin resistance protein [imported] - Brucella melitensis (strain 16) C;Species: Brucella melitensis (c;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002 C;Accession: AG3547
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A; Residues: 1-197 < ARN>
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D.; Let
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probable cysteine synthase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Date: 17-Jul-1998 #text_change 20-Jun-2000
C;D
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C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: D83080
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hic adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lar
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C71132
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LOTY, S., Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa
A;Title: Complete genome sequence of Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PH0824 · Pyrococcus horikoshii C;Speckes: Pyrococcus horikoshii C;Speckes: Pyrococcus horikoshii C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000 C;Accession: C71132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: C71132
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A; Residues: 1-278 <STO>
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8; Conser
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Y.; Funahashi, T.;
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K.; Lim,
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                                                                                                                                                                                                                                                                                                                                               R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, h; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
                                                                                                            A;Cross-references: GB:AE008689; PIDN:AAL44750.1; PID:g17742385; GSPDB:GN00187
                                                                                                                                                                                                                    A; Reference number: A; Accession: AH3041
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                                A; Gene:
                                                              C; Genetics:
                                                                                    A; Experimental source:
                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-381 <KUR>
                                                                                                                                                                                            A;Status: preliminary
                                                                                                                                                                                                                                               A; Title: The Genome of the Natural A; Reference number: AB2577; PMID:1:
                                                                                                                                                                                                                                                                                                   ster, E.W.
                                                                                                                                                                                                                                                                                                                      A; Authors: Yoo, H.;
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linear

strain

C58

(Dupont)

Y.; Biddle,

P.;

Jung,

X

Krespan, W.;

Perry, M.; Gordon-Kam

WOO

Natural Genetic PMID:11743193

Engineer

Agrobacterium

tumefaciens C58

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A; Molecule type: DNA
A; Residues: 1-372 <COL>
A; Cross-references: GB:AL022004; GB:AL123456;
A; Experimental source: strain H37Rv
C; Genetics:
conserved hypothetical protein Atu3948 [imported] - Agrobacterium tumefacie
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                               A;Map position: REV7250-6111
C;Superfamily: formate dehydrogenase chain B;
C;Keywords: oxidoreductase
E;273-348/Domain: ferredoxin 2[4Fe-4S] homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.;
A;Title: Complete genome sequence of the methanogenic archaeon, Met
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: E64300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C;Accession: E64300
                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:U67459; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutt; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: cysM3
C;Superfamily: threonine
                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-379 <BUL>
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Best Local
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nilarity 100.0%;
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Pred. No.
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RESULT 14
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   sperm-binding glycoprotein
N;Alternate names: sperm re
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A;Title: Genome Sequence of the Plant Pathogen and A;Reference number: A97359; PMID:11743194
A;Accession: D98244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein AGR_L_1808 [imported] - Agrobacterium tumefaciens (strain C;Species: Agrobacterium tumefaciens C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
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A;Molecule type: DNA
A;Residues: 1-387 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein At2g45000 [imported] - Arabidopsis thaliana (c;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84885
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A;Gene: AGR_L_1808
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A; Residues: 1-397 < KUR>
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yegB
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C;Species: Mesocricetus auratu
C;Sate: 10-Sep-1999 #Sequence.
C;Aate: 10-Sep-1999 #Sequence.
C;Accession: A60503
R;Kinloch, R.A.; Ruiz-Seiler,
Dev. Biol. 142, 414-421, 1990
                                                                                                                                                           C:Species: Yersinia pestis
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 17-May-2002
C:Accession: AC0347
C:Accession: AC0347
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:AL117414
A;Experimental source: fetal kidney;
C;Genetics:
A;Note: DKFZp5660011.1
C;Superfamily: gamma-glutamyltransfer
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A;Note: the authors translated the codon CAA for residue 251 as Glu, C;Comment: This sulfated glycoprotein in the zona pellucida of the or C;Superfamily: sperm-binding glycoprotein ZP3; ZP domain homology C;Keywords: glycoprotein; oocyte F;45-300/Domain: ZP domain homology <ZPH>
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Jun-2000
C;Accession: T17220
C;Accession: T17220
R;Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18725
A;Reference number: T17220
A;Recession: T17220
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                     A; Molecule type: DNA
A; Residues: 1-465 < KUR>
                                                                                        A; Reference number: AB0001; A; Accession: AC0347
                                                                                                             A; Title: Genome sequence of Yersinia pestis, A; Reference number: AB0001; MUID:21470413; P
                                                                                                                                                                                                                                                                                                     probable membrane protein yegB [imported] - Yersinia pestis (strain CO92)
C; Species: Yersinia pestis
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A; Residues: 1-443 <BLU>
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A; Residues: 1-422 <KIN>
                                                                  A; Status: preliminary
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Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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les 8; Conserv
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GB:AL590842; PIDN:CAC92102.1; PID:g15980820; GSPDB:GN00175
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probable ATP-binding transport protein HI1156 - Haemophilus influenzae (strain Rd KW20) C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 02-Feb-2001
C;Accession: E64186
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
                                                                                                                                                     A;Cross-references: GB:U32795; GB:L42023; NID:g1574708; IC;Superfamily: unassigned ATP-binding cassette proteins; C;Keywords: ATP; nucleotide binding; P-loop F;355-50/Domain: ATP-binding cassette homology <ABC>F;372-379/Region: nucleotide-binding motif A (P-loop)
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A;Molecule type: DNA
A;Residues: 1-576 <TIGR>
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E64186
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Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable transport protein - Deinococcus radiodurans (strain R1) C;Speciles: Deinococcus radiodurans (c;Speciles: Deinococcus radiodurans (c;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000 C;Accession: A75267 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; D
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A; Residues: 1-471 <WHI>
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    PLALGLGL 166
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100.0%; Pr
                                                                        100.08; F
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21;
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5. 25;
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Zalewski,
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С.; Ма
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C;Accession: D58208
R;Hunt, J.G.; Kasinsky, H.E.; Elsey, R.M.; Wright, C.L.;
J. Biol. Chem. 271, 23547-23557, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma-glutamyltransferase (EC 2.3.2.2) related protein - humar N;Alternate names: gamma-glutamyltransferase-like activity 1; C;Species: Homo sapiens (man) C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_chang C;Accession: A41125
                                                                    R:Queralt, R.; Oliva, R.
Nucleic Acids Res. 19, 5786, 1991
A;Title: Protamine 1 gene sequence from the primate Saguinus
A;Reference number: S22582; MUID:92051332; PMID:1840669
A;Accession: S22582
                                                                                                                                                                                               C;Species: Saguinus imperator
C;Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 21-Jul-2000
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A; Residues: 1-45 <HUN>
C; Superfamily: sperm hist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 271, 23547-23557, A;Title: Protamines of reptiles. A;Reference number: A58208; MUID A;Accession: D58208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protamine II-3 - painted turtle
C;Species: Chrysemys picta (painted turtle)
C;Date: 08-Nov-1996 #sequence_revision 08-Nov-1996 #text_change 07-May-1999
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C; Keywords:
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A; Residues: 1-586 <HEI>
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A;Title: Identification of a human gamma-glutamyl cleaving enzyme related 1 A;Reference number: A41125; MUID:91296809; PMID:1676842
A;Accession: A41125
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A;Cross-references: EMBL:X61678; NID:g58405; PIDN:CAA43853.1; PID:g4494091
A;Note: the authors translated the codon TAC for residue 43 as Thr
                                       A; Molecule type: DNA
A; Residues: 1-50 <QUE>
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Matches
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Best Local
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; Pred. No.
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26;
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A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87604
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C:Species: Didelphis virginiana, Didelphis marsupialis virginiana
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23
C:Accession: S34045
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C;Superfamily: sperm histone
C;Keywords: chromosomal proto
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A;Title: Characterization of a marsupial sperm protamine gene A;Reference number: S34045; MUID:93345500; PMID:8344286
A;Accession: S34045
protein ZC334.3 [imported] - Caen
C; Species: Caenorhabditis elegans
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A; Residues: 1-86 <STO>
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A; Residues: 1-58 (WIN)
A; Cross-references: EMBL: X74044;
C; Superfamily: sperm histone
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Best Local
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                  Caenorhabditis
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Pred. No. 32;
0; Mismatches
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                                                                                                                                                                                                             DB 2;
                  elegans
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                                                                                                                                                                                                                                                                                PIDN: AAK24834.1; GSPDB: GN00148
                                                                                                                                                                          0;
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                                                                                                                                                                                                           Length 86;
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23-Jul-1999
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                                A; Experimental
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A; Molecule type: DNA
A; Residues: 1-115 <RAS>
A; Residues: 1-115 <RAS>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 32-115/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (clone VH32) C;Species: Homo sapiens (man) C;Date: 05-Aug-1994 #sequence_revision C;Accession: PH1560
                                                                                                                                        C; Accession: H83201
R; Stover, C.K.; Pham, X.Q.; adman, S.; Yuan, Y.; Brody, .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                              conserved hypothetical protein PA3557 [imported] - Pseudomonas aeruginosa (:
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Lack of extensive mutations in the VH5 genes used A;Reference number: PH1557; MUID:93210459; PMID:7681468 A;Accession: PH1560
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A;Residues: 1-102 <STO>
A;Cross-references: GB:chr_I; PIDN:CAB04964.1; PID:g3881432; GSPDB:GN00019; CESP:ZC33
A;Cross-references: GB:chr_I; PIDN:CAB04964.1; PID:g3881432; GSPDB:GN00019; CESP:ZC33
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Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode C. elegans: a platform for investigating bio A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Rassenti, L.Z.; Kipps, T.J. J. Exp. Med. 177, 1039-1046, 1993
                       A; Molecule type: DNA
A; Residues: 1-115 <STO>
                                                                                A; Reference number: A82950; A; Accession: H83201
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A;Cross-references: GB:AE004776; GB:AE004091; NID:g9949701; PIDN:AAG06945.1;
                                                           A; Status: preliminary
                                                                                                                         A; Title: Complete genome
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                                                                                                        sequence of Pseudomonas aeruginosa 50; MUID:20437337; PMID:10984043
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L.L.; (
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RESULT 28
AE1753
Orf51 [bacteriophage bIL285] homolog lin2570 [imported] - Listeria innocua
C;Species: Listeria innocua
C;Species: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                      A;Cross-references: GB:AL592022; PIDN:CAC97797.1; PID:g16415092; GSPDB:GN00178 A;Experimental source: strain Clip11262 C;Genetics:
                                                                                                                                                                                                                              D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maduenc ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1753
                                                                                                                                                                                                                                                                                                                                       C;Accession: AE1753
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, .: Dominguez-Bernal, G.; Duchaud, E.; Durand, L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Engler, J.A.; van Bree, M.P.
Gene 14, 155-163, 1981
A;Title: The nucleotide sequence and protein-coding capability
A;Reference number: A03582; MUID:82028652; PMID:6269958
A;Accession: C03582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 10-Sep-1999
C;Accession: B91483; C03582; A04466
R;Schoner, B.; Kahn, M.
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A; Residues: 1-118 <GLA>
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C; Superfamily: Esc
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A; Residues: 1-118 <EN
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A;Title: The nucleotide sequence of IS5 from Escherichia
A;Reference number: A91483; MUID:82028653; PMID:6269959
A;Accession: B91483
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Pred. No. 57;
0; Mismatches
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Pred. No.
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59;
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Voss, H.; Wehland
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002 C;Accession: AH2707 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefacier
                                                  R;Lakkis, F.G.; Cruet, E.N.
Biochem. Biophys. Res. Commun. 197, 612-618, 1993
A;Title: Cloning of rat interleukin-13 (IL-13) cDNA and
                                                                                                                                                                                                                                                                                                                                                                     A; Map position:
A; Introns: 99/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-125 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A; Accession: T27519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 2C334.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t. C;Accession: T27519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein Atul065 [imported] - Agrobacterium tumefaciens C; Species: Agrobacterium tumefaciens
                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z82082; PIDN:CAB04964.2; GSPDB:GN00019; CESP:ZC334.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, A; Reference number: Z20381
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A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-123 <KUR>
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A;Accession: AH2707
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100.0%; Pred. No. 61
ive 0; Mismatches
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of IL-13 gene expres
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RESULT 32
E30552
T-cell activation protein P600 precursor - mouse
T-cell activation protein P600 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change
C:Accession: E30552
R:Brown, K.D.: Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
T. Immunol. 142, 679-687, 1989
T. Immunol. 142, 679-681 inducible proteins secreted by leuko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: 152290; MUID A;Accession: 152290
A;Status: preliminary; translate: A;Molecule type: mRNA A;Residues: 1-131 <RES> A;Cross references: GB:L26913; N. C;Genetics:
밁
                                                                                                                                                                                                                            probable transposase, truncated [imported] - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 15-Sep-2000 C;Accession: T37116
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Re submitted to the EMBL Data Library, August 1999
A;Reference number: Z2158
A;Accession: T37116
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Immunol. 142, 679-687, 1989
A:Title: A family of small inducible proteins secreted by sof various activation processes.
A:Reference number: A30552; MUID:89093958; PMID:2521353
A:Accession: E30552
A:Molecule type: mRNA
A:Residues: 1-131 <BRO>
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                                                                                                                      C; Superfamily:
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C;Superfamily: interleukin-13
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C;Superfamily:
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A; Residues: 1-146 <SAU>
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Best Loc
Matches
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Best Local
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102
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LGLLLAV 108
                           LGLLLAV 76
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                                                                       Score 7;
Pred. No
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                                                          red. No. 70 Mismatches
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70;
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64;
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                        A; Reference number: A; Accession: S31078
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A; Note: DKF
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C;Superfamily:
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sed allergen RA5 - rice
sed allergen RA5 - rice
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Date: 31078
C;Accession: S31078
R;Adachi, T; Izumi, H.; Yamada, T.; Tanaka, K.; Takeuchi, S.; N
R;Adachi, T.; Izumi, H.; Yamada, T.; Tanaka, K.; Takeuchi, S.; N
Plant Mol. Biol. 21, 239-248, 1993
Plant Mol. Biol. 21, 239-248, 1993
                                                                                Plant Mol. Biol. 21, 239-248, 1993
A;Title: Gene structure and expression of rice seed allergenic
A:Reference number: S31078; MUID:93144699; PMID:7678765
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A;Title: Complete sequence and gene organization of the genome of a A:Title: Complete sequence and gene organization of the genome of a A:Paference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the Protein Sequence A; Reference number: Z16474 A; Accession: T08734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Homo sapiens (man)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change
C:Accession: T08734
  A;Cross-references:
C;Superfamily: wheat
                                       A; Molecule type: mRNA
A; Residues: 1-157 <ADA>
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A; Residues: 1-150 <OT
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A; Residues: 1-147 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein PH2001 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: A71217
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A71217
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EMBL:D11430; NI
t alpha-amylase
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Tanaka, T.; Kudoh, Y.;
  NID:g218196;
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Pred. No.
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o. 72;
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o. 71;
                   PIDN:BAA01996.1; PID:g218197
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Yamazaki,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                          proteins belonging
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Kushida,
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RESULT 38
A75567
A75567
Conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C.Species: Deinococcus radiodurans
C.Species: Deinococcus radiodurans
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C.Accession: A75567
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C.Accession: A7567
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T02664
                                                                                                                                                                                                                                                                                                                                                                                              R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:AF042200; NID:g2827315; PIDN:AAB99797.1; A;Experimental source: strain Nipponbare C;Superfamily: wheat alpha-amylase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allergen - rice
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Jul-1999
hypothetical protein . C; Species: Deinococcus
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                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-157 <WHI>
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A; Residues: 1-157 <YUN>
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A; Description: Nucleotide sequence of rice allergenic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Yun, C.H.; Park, J.H.; Eun, M.Y. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T02664
R; Yun, C.H.; Park,
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                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE001867;
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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A; Accession: T02664
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ilarity 100.0%;
Conservative (
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 Deinococcus radiodurans
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                                                                                                                                                                                                                                                                                                                                                                                                                   the radioresistant bacterium Deinococcus radiodurans R1 \, MUID:20036896; PMID:10567266
                                                                                                                                                                                                   Score 7; ; Pred. No
                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                           GB:AE000513; NID:g6457693; PIDN:AAF09626.1; PID:g645769
                    radiodurans (strain R1)
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11 LLLAVVS

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Search completed: March Job time: 47 secs

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2003,

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RESULT 40
S59925
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Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75530
                                                                                                                                                                            A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-160 <ALV>
                                                                                                                                                                                                                                            R;Alvarez, A.M.; Adachi, T.; Nakase, M.; Aoki, N.; Nakamura, R.; Matsuda, T. Biochim. Biophys. Acta 1251, 201-204, 1995
A;Title: Classification of rice allergenic protein cDNAs belonging to the alpha-amyla A;Reference number: S59922; MUID:95399441; PMID:7669811
A;Accession: S59925
                                                                                                                                                                                                                                                                                                                                                        C:Species: Oryza sativa (rice)
C:Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 20-Jun-2000
C:Accession: S59925
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A; Molecule type: DNA
A; Residues: 1-157 <WHI>
δÃ
                                                                                                                                A;Cross-references: EMBL:D42142; NID:g1398917; C;Superfamily: wheat alpha-amylase inhibitor
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C;Accession: E75530
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Best Local Similarity
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T.; Zalewski,
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length: 2000000000
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Match
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                   Length
 В
TN12_HUMAN
TN12_MOUSE
YEBW_ECOLI
PSAB_ODOSI
PSAB_CUCA
ADHS_GLUCA
ADHS_GLUCA
ADHS_GLUCA
ADHS_GLUCA
ADHS_GLUCA
ADHS_GLUCA
CYDC_HAEIN
GGT5_HUMA
HSP1_SAGIM
HSP1_SAGIM
HSP1_SAGIM
HSP1_STAGIM
HSP1_STAGIM
HSP1_STAGIM
HSP1_STAGIM
HSP1_SCOLI
IL13_MOUSE
IL13_RCT
YK01_PYRHO
TNFC_PIG
TNFC_COXBU
RNFC_FOYBU
RNFC_FOYBU
RNFC_COXBU
TN114_MOUSE
TN114_MOUSE
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054907 mus musculu
047377 escherichia
p49480 odontella s
09t196 cyanidium c
09t544 gluconobact
08yd73 brucella me
09tuk4 pan troglod
060316 methanococc
p23491 mesocricetu
p45081 haemophilus
p35269 homo sapien
p24714 saguinus im
p35305 didelphis m
046202 drosophila
p03838 escherichia
p03838 escherichia
p20109 mus musculu
p42203 rattus norv
Q8zed4
Q57020
Q9qyh9
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Q8xex9
P58344
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        7 ovis aries
9 salmonella
4 escherichia
9 escherichia
7 coxiella bu
4 yersinia pe
haemophilus
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7 escherichia
8 caenorhabdi
5 bubalus bub
6 capra hircu
                                                                                                                 pyrococcus
sus scrofa
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ALIGNMENTS

[3] SEQUENCE FROM N.A.		ĉ
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Biol. 8:525-528(1998).	Apos.	2 3
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	Ashke	RA
rs S.A., Sheridan J.P., Pitti R.M., Brush J., Goddard A.	Marsters	RΑ
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Primates; Catarrhini; Hominidae;	Mamma	88
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PROSITE; PS50049; Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lynch C.N., Wang
 216
                           121
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                                                                                                                                                      36 MAARRSQRRRGERGEPGTALLVPLALGLGLALACLGLLLLAVVSLGSRASLSAQEPAQEEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by proteolytic processing.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
SIMILARITY: Become differs from that shown due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMOTRIMER (POTENTIAL).
SUBCELLULAR LOCATION: Type II membrane protein and secreted.
TISSUE SPECIFICITY: Highly expressed in adult heart, pancreas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch C.N., Wang Y.C., Lund J.K., Chen Y.-W., EAK induces angiogenesis and proliferation Biol. Chem. 274:8455-8459(1999). FUNCTION: Binds to FN14 and possibly also inducer of apoptosis in some cell types. M activation. May promote angiogenesis and t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lung and brain.
PTM: The soluble form derives
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                                          GAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD
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SIGNAL-ANCHOR (TYPE-II MEMBRANE
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E660843361C28EBA CRC64;
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the proliferation of
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RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Blake J., Boffelli D., Bojunga N., Carnici P., de Bonaldo M.F.,
RA Boromstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H. Saro K. Schoenbach C. Schoenbach C.
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily membinducer of apoptosis) (TWEAK) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                            Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
-!- FUNCTION: Binds to FN14 and possibly also to TNRFSF12/APO3.
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[2]
                                  This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Peritoneal macrophage;

MEDLINE-98070415; PubMed-9405449;

Chicheportiche Y., Bourdon P.R., Xu H., Hsu Y.-M., Scott H.,

Hession C., Garcia I., Browning J.L.;

"TWEAK, a new secreted ligand in the tumor necrosis factor family that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 83-225 FROM N.A. STRAIN-C57BL/6J; TISSUE-Retina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Mammalia; Eutheria;
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J. Biol. Chem.
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                                                                                      PTM: The soluble form is produced from the membrane form proteolytic processing (By similarity).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                      TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                               similarity)
                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Type
                                                                                                                                                                                                                                                                          SUBUNIT: Homotrimer (Potential).
                                                                                                                                                                                                                                                                                                         activation (By similarity).
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SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
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272:32401-32410(1997).
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                                                                   This
                                                                                                           Sharma V., Hudspeth M.E., Meganathan R.; "Menaquinone (vitamin K2) biosynthesis: characterization of the menE gene from E
                                                                                                                                                                                                                     Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat Hypothetical protein yfbw.
                      modified
                                             the
                                                                                                   Gene
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                                                                                                                                                        STRAIN-K12
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MEDLINE=97426617; PubMed=9278503;
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STRAIN-K12 / MG16
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SMART; SM00207; TNF; 1
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                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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European Bioinformatics Institute. They by non-profit institutions as long a lifted and this statement is not removed. Ities requires a license agreement (See lead of an email to license@isb-sib.ch).
                                                                                   SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                              B., Shao Y.;
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PS50049;
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                                                      the Swiss Institute of Bioinformatics
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RESULT 4
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EMBL; L35031; AB04895.1; -.
Ecodene; EG14344; Y1bW.
InterPro; IPR000620; DUF6.
                                                                                                                                                    or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biddulphiophycidae;
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15-JUN-2002
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01-FEB-1996
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Hypothetical protein; Transmembrane;
TRANSMEM 36 56 POTENTI.
          Iron-sulfur;
TRANSMEM
                                    Photosynthesis; Photosystem I; Transpo:
Chloroplast; Thylakoid; Transmembrane;
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PRINTS; PR00257; PHOTSYSPSAAB.
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HSSP; P25897; 1JBO.
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                                                            PROSITE; PS00419;
                                                                                                   InterPro; IPR001280; PSI_PsaA/B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 LGLALACLGL
                                                                                                                                                                                                                                                     thylakoid membrane.
SIMILARITY: BELONGS TO THE PSAA/PSAB FAMILY.
                                                                                                                                                                                                                                                                              SUBUNIT: A psaA/B heterodimer binds the P700 chlorophyll special pair and subsequent electron acceptors. The PSI reaction center higher plants and algae is composed of one at least 11 subunits. SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
                                                                                                                                                                                                                                                                                                                                                                     nt Mol. Biol. Rep. 13:336-342(1995).
FUNCTION: PsaA and psaB bind P700, the primary electron donor of photosystem I (PSI), as well as the electron acceptors AO, AI, photosystem I (PSI), as well as the electron acceptors AO, AI, FX. PSI functions as a plastocyanin/cytochrome c6-ferredoxin
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                                                                                                                                                                                                                                                                                                                                 is a phylloquinone and FX is a 4Fe-4S iron-sulfur center.
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                                          PHOTOSYSTEM_I_PSAAB; 1.
hotosystem I; Transport; Electron transport;
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41, Last annotation
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                                                                                                                                                              license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                         s SWISS-PROT entry is copyright. It ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                              COFACTOR: P700 is a chlorophyll A dimer, A0 is chlorophyll A, A1 is a phylloquinone and FX is a 4Fe-4S iron-sulfur center. SUBUNIT: A psaA/B heterodimer binds the P700 chlorophyll special pair and subsequent electron acceptors. The PSI reaction center higher plants and algae is composed of one at least 11 subunits. SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast
                                                                                                                                                                                              thylakoid membrane.
SIMILARITY: BELONGS TO THE PSAA/PSAB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: PsaA and p
photosystem I (PSI),
Fx. PSI functions as
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(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
I P700 chlorophyll A apoprotein A2
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XI (POTENTIAL).

IRON-SULFUR FX (4FE-4S) (BY SIMILARITY).

IRON-SULFUR FX (4FE-4S) (BY SIMILARITY).

P700 SPECIAL PAIR CHLOROPHYLL AXIAL

LIGAND (BY SIMILARITY).

AO CHLOROPHYLL (BY SIMILARITY).

AO CHLOROPHYLL (BY SIMILARITY).

A1 PHYLLOQUINONE (BY SIMILARITY).

A1 PHYLLOQUINONE (BY SIMILARITY).
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ns as long as its content
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or send an email to license@isb-sib.ch)

(See http://www.isb-sib.ch/announce/

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restrictions

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ADHS_GLUOX
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Best Local
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                 ADHS
                                                                                                   - I FUNCTION: NOT ESSENTIAL FOR ALCOHOL DEHYDROGENASE ACTIVITY.

- I SUBUNIT: HETEROTRIMER (DEHYDROGENASE, CYTOCHROME AND PROTEIN
ADHS), THAT FORMS THE ALCOHOL DEHYDROGENASE COMPLEX.

- I SUBCELLULAR LOCATION: MEMBRANE-BOUND, FACING THE PERIPLASMIC
                                                                                                                                                            expression in Acetobacter pasteurianus."; Appl. Environ. Microbiol. 63:1131-1138(1997)
                                                                                                                                                                                                                                                                                                                    Gluconobacter oxydans (Gluconobacter suboxydans).
Bacteria; Proteobacteria; alpha subdivision; Acetobacteraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00419; PHOTOSYSTEM_I_PSAAB; 1.
Photosynthesis; Photosystem I; Transport; Electron transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00223; psaA_psaB; 1. PRINTS; PR00257; PHOTSYSPSAAB
                                                                                                                                                                                        bound alcohol dehydrogenase from Gluconobacter
                                                                                                                                                                                                     "Characterization of the genes encoding
                                                                                                                                                                                                                    Kondo K., Horinouchi
                                                                                                                                                                                                                                  MEDLINE=97208225; PubMed=9055427;
                                                                                                                                                                                                                                                 STRAIN-IFO 12528;
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                                                                                    SPACE (POTENTIAL).
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4Fe-4S; Ch
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A1 PHYLLOQUINONE (BY SIMILARITY).

A1 PHYLLOQUINONE (BY SIMILARITY).
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                                                                                                                                                                                      Hypothetical
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=16M / ATCC 23456 / Biotype 1;
MEDLINE=20020109; PubMed=11756688;
DelVecchio V.G. Kapatral V., Redkar R.J., Patra G., Mujer Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Rez Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letessor Haselkorn R., Kyrpides N., Overbeek R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein BMEII0304.
                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                              use
                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                                                                                        Brucella melitensis.";
Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                           Haselkorn R., Kyrpides N., Overbeek R., The genome sequence of the facultative intracellular pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=16M / ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
Brucellaceae; Brucella.
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15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
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Q8YD73;
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                                           132 ALLVPLAL 139
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                                                                54 ALLVPLAL 61
                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO THE UPF0191 FAMILY.
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                                                                                                                              Protein; 20 3; 54 7; 85 10 124 14 153 17 179 15 220 AA; 7
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last anotation update)
Melanocyte stimulating hormone receptor (MSH-
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan
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C., Dixon C., Matthews J.N., Sajantila A
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01-NOV-1997
15-JUN-2002
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                           METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanocaldococcaceae; NCBI_TaxID=2190;
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Matches
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                                               CYDC_HAEIN P45081;
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CARBOHYD
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InterPro; IPR001507; Endoglin/CD105.
Pfam; PF00100; zona_pellucida; 1.
PRINTS; PR00023; ZPELLUCIDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long a
modified and this statement is not removed;
entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuuse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinloch R.A., Ruiz-Seller B., Wassarman P.M., "Genomic organization and polypeptide primary pellucida glycoprotein hzP3, the hamster sperr Dev. Biol. 142:414-421(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00023; SMART; SM00241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zona pellucida sperm-binding protein 3 precursor (Zona pellucida glycoprotein ZP3) (Sperm receptor) (Zona pellucida protein C).
                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00682; ZP_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91078540; PubMed=2257975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mesocricetus auratus (Golden
                                                                                                                                          386
                                                                                                                                                                       59 LALGLGLA
                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEVELOPMENTAL STAGE: GROWING OOCY PTM: SULFATED GLYCOPROTEIN WITH O SIMILARITY: CONTAINS 1 ZP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSI SPERM-ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUT SPECIES-SPECIFICITY OF THE INSEMINATION.
SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: OOCYTES
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8; Conser
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23
387
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422 AA;
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Rodentia;
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                                                                                                                                                                                                                       Pred.
                                                                 PRT;
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-LINKED (GLCNAC. . .) (PO-
-LINKED (GLCNAC. . .) (PO-
DOF95BE7FF8E7E01 CRC64;
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6; 1:
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n receptor
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GGT5_HUMAN S
P36269; Q96FC1;
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MEDLINE-9535630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM TRANSMEM
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Pfam; PF00664; ABC_membrane;
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InterPro; IPR003439; ABC_transportr.
InterPro; IPR001140; ABCtranprtrTM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U32795; AAC22811.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Executive Buropean Bioinformatics Institute. There are no restance.
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SIMILARITY: BELONGS TO
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8; Conser
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                                                                  STANDARD;
29,
29,
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153
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TO BE A COMPONENT OF A TRANSPORT
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sequence update)
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-!- FUNCTION: CAN HYDROLYZE THE GAMMA-GLUTAMYL MOIETY OF GLUTAMYL AS WELL AS CONVERT LEUKOTRIENE C4 TO LEUKOTRIENE D4.
-!- CATALYTIC ACTIVITY: (5-1-91Ltamy1)-peptide + an amino ac: peptide + 5-L-91Ltamy1-amino acid.
-!- SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, SYNTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE SIMILARITY).
-!- SUBCELLULAR LOCATION: Type II membrane protein (Probable)-
-!- SUBCELLULAR LOCATION: Type II membrane protein (Probable)-
-!- SIMILARITY: STRONG, TO OTHER GGT ENZYMES AND TO GL-7ACA /-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Last annotation update) Gamma-glutamyltranspeptidase 5 precursor (EC glutamyltransferase 5) (GGT-Rel).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
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PRINTS; PR01210; GGTRANSPTASE.
PROSITE; PS00462; G_GLU_TRANSPEPTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew; HGNC:4260; GGTLA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; BC011362; AAH11362.1; PIR; A41125; A41125.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See.http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eventhe European Bioinformatics Institute. There are no restricted the succession of the successi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glutamyltransferase GGTLA1 OR GGT5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; T03.002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of a human gamma-glutamyl cleaving but distinct from, gamma-glutamyl transpeptidase.", Proc. Natl. Acad. Sci. U.S.A. 88:6303-6307(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Groffen J
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s (Human).
Metazoa; Chordata; C
Metazoa; Primates; (
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Rajpert-De Meyts
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TO OTHER GGT ENZYMES AND TO GL-7ACA ACYLASES.
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Pred. No
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SIGNAL-ANCHOR (TYPE-II
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                                                                                                                         1BE543CB0934B16B
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DT 01-FEB
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Best Local :
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01-FEB-1994
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P35305;
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p1R; S22582; S22582.
InterPro; IPR000221; Protamine_Pl.
pfam; PF00260; protamine_Pl; 1.
pROSITE; PS0048; PROTAMINE_Pl; 1.
Chrosite; PS0048; PROTAMINE_Pl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sperm protamine
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  Didelphis marsupialis Monodelphis domestica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (S or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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01-MAR-1992 (Rel. 21, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSP1_SAGIM P24714;
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                                                                  (Rel. 2)
(Rel. 2)
(Rel. 4)
mine Pl.
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                                                                                                                                                                               STANDARD;
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Primates;
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  virginiana (North American
(Short-tailed grey opossum)
                                                                                      sequence update) annotation updat
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Best Local S
Matches 7
                                                                                                           Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

MCBI_TaxID=7227;
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046202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Retief J.D., Krajewski C., Westerman M., Winkfein R.J., Dixon G.H.;
"Molecular phylogeny and evolution of marsupial protamine P1 genes.",
Proc. R. Soc. Lond., B, Biol. Sci. 259:7-14(1995).
-1- FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHROMATIN OF
SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY COMPACT
SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE COMPLEX.
-1- SUBCELLULAR LOCATION: Nuclear.
-1- TISSUE SPECIFICITY: TESTIS.
-1- SIMILARITY: BELONGS TO THE PROTAMINE P1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES=D.marsupialis;
MEDLINE=93345500; PubMed=8344286;
Winkfein R.J., Nishikawa S., Connor W.,
SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY STRAIN=Canton-S; TISSUE=Male accessory gland; MEDLINE=98135120; PubMed=9474779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding; Testis; DNA condensation; Nuclear protein.
INIT_MET 0 BY SIMILARITY.
SEQUENCE 57 AA; 7810 MW; 283715B280214E52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000221; Protamine_P1.
Pfam; PF00260; protamine_P1; 1.
PROSITE; PS00048; PROTAMINE_P1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L17007; AAA02812.1; -. EMBL; X74044; CAA52193.1; -. EMBL; L35448; AAA74612.1; -. PIR; S34045; S34045.
                                                                                                                                                                                                                                                                 Accessory gland protein Acp62F ACP62F OR CG1262.
                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcripts from the North American opossum (Didelphis marsupialis).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of a marsupial sperm protamine ge transcripts from the North North
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No.
                                                                                                                                                                                                                                                                                                precursor.
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RA Glodek A. Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeqwam C.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeqwam C.,

RA Harris N.L., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Herkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Rahert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spler E., Spradling A.C., Stapleton M., Skupskin M.P., Smith T.,

RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Yeb J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

RT The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                    This SWI
between
                                                                                                                                                                                                                                                                                                                     Drosophila.; Genetics 156:1879-1888(2000).

Genetics 156:1879-1888(2000).

-i- FUNCTION: RESPONSIBLE FOR PHYSIOLOGICAL AND BEHAVIORAL CHANGES MATED FEMALE FILES. MAY CONTRIBUTE TO THE TOXICITY OF SEMINAL FLUID AND THE DECREASED LIFE-SPAN OF MATED FEMALES. MAY ALSO AFFERT NEUROMUSCULAR EVENTS AFTER MATING CONCERNING SPERM STOR
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Durbin
Fosler
Glodek
Harris
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Durbin K.J., Evangelista C.C., Ferrag C., Ferriera S., Fleischmann W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayan B., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Beallow P. B., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Various strains;
MEDLINE=20556153; PubMed=11102381;
Begun D.J., Whitley P., Todd B.L., Wald
"Molecular population genetics of male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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Drosophila.":
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                                                                                                                 European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Secreted (Probable). TISSUE SPECIFICITY: SEMINAL FLUID.
                                                                                                                                                                                                                                             SIMILARITY:
                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.F., Harada H.A., Bertram M.J., Stelick T.J., Kraus K.W., M., Lung Y.O., Neubaum.D.M., Park M., Tram U.K.; nes for male accessory gland proteins in Drosophila
                                           s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                non-profit institutions as long and this statement is not removed. requires a license agreement (See
AAB96387.1;
                                                                                                                                                                                                                                             SOME,
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                                                                                                                                                                                                                                             P. NIGRIVENTER TX2-6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          accessory gland
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                                                                                                                                           restrictions
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Best Local
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                                                                                                         Takemoto K.,
Yamamoto Y.,
Ichihara S.,
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P03838;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                               SEQUENCE FROM N.A. STRAIN=K12;
                                                                                                                                                                                                                                                                                                                     "The nucleotide sequence transposable element IS5. Gene 14:155-163(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Escherichia.
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MEDLINE=97251357;
Aiba H., Baba T.,
                                                                                                                                                          STRAIN=K12;
                                                                                                                                                                                                                         Davis R.W.;
                                                                                                                                                                                                                                                      Davis K.,
                                                                                                                                                                                                                                                                                                                                                                   Engler J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schoner B., Kahn M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-82028653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insertion element 
Escherichia coli.
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                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                      Lashkari D., Lew
                                                                                                                                                                                                                                                                          Schramm
                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=82028652;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleotide sequence 14:165-174(1981).
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AY010616;
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AY010611;
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AY010609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF01826; TIL;
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                                                                                                                                                                                                                                                                                      FROM N.A.
                                                                                                                                                                                                                                                      Federspiel
                                                                                                                                                                                                          (SEP-1996)
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115 /
                                                                                                    Mori H., A., Inokuchi H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel.
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AAG35370.1;
AAG35371.1;
AAG35372.1;
AAG35373.1;
AAG35374.1;
AAG35375.1;
AAG35376.1;
AAG35376.1;
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AAG35367.1;
AAG35368.1;
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41,
1S5
PubMed=9097039;
Fujita K., Hayashi K.,
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115
12570
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Lin
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H., Miki
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I., Hyman R.
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ACCESSORY GLAND PROTEIN A

MW; 4326AA6F6C32291D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma subdivision; Enterobacteriaceae;
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annotation update)
hypothetical 12 kD
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                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
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Namath A., Oefner
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Nakata
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S., Komp C., Kurd
fner P., Roberts |
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P SEQUENCE FROM N.A.

MEDLINE-89093958; PubMed-2521353;

A Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;

A family of small inducible proteins secreted by leukocytes and members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and Tibroblast-derived inflammatory cytokine product of Function: Cytokine Inhibits Inflammatory and Immune Richard Company and Immune Ri
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"A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage ma DNA Res. 3:363-377(1996).
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EMBL; D83536;
EMBL; D90771;
EMBL; D90772;
EMBL; D90841;
EMBL; D90847;
EMBL; D90847;
EMBL; D90848;
PIR; D44466;
PIR; D44666;
PIR; D44666;
PIR; D4466
                                                                                              This
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                                    the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Interleukin-13 precursor (IL-13) (T-cell acti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
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L; U70214; AAB08680.1; -
L; D83556; -; NOT_ANNOTATED_CDS.
L; D90771; BAA14925.1; -
JL; D90772; BAA14935.1; -
JL; D90841; BAA15715.1; -
JL; D90841; BAA1572.1; -
JL; D90847; BAA15972.1; -
JL; D90848; BAA15983.1; -
BL; D90848; BAA15983.1; -
R; A04466; IEEC5B.
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      European
by non-
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SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
                        SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL European Bioinformatics Institute. There are no restrict
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Hal protein; 118 AA; 12:
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ilarity 100.0%;
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Rodentia;
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(See http://www.isb-sib.ch/announce/
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RESULT 18
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                                                         EMBL; L26913;
HSSP; P35225;
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      IPR003634;
IPR001325;
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IL13_RAT PF
P42203;
O1-NOV-1995 (Rel. 32, Created)
O1-NOV-1995 (Rel. 32, Last seque
15-7UL-1998 (Rel. 36, Last annot
Interleukin-13 precursor (IL-13)
IL13 OR IL-13
                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning of rat interleukin-13 (IL-13) cDNA and analysis of IL-13 gene expression in experimental glomerulonephritis."; Biochem. Biophys. Res. Commun. 197:612-618(1993).
-!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION. SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS. MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-Sprague-Dawley; TISSUE-Kidney commEDITINE-94092138; pubMed-7916615; Lakkis F.G., Cruet E.N.; "Cloning of rat interleukin-13 (IL-13) "Cloning of rat interleukin-13 (ID-13) gene expression in experimental glomer procession in experimental glower procession in experimental glower procession in experimental 
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PIR; E30552; E30552.
HSSP; P35225; 3ITR.
MGD; MGI:96541; I113.
InterPro; IPR0013634; Interleukin_13.
InterPro; IPR001325; Interleukin_4_13.
Pfam; PF03487; Interleukin_13; 1.
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                                                                                                 entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
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Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
NCBI_TaxID=10116;
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PROSITE; PS00838; INTERLEUKIN_4_13; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
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Rodentia;
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(IL-13) (T-cell activation
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Pred. No. 29;
0; Mismatches
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29;
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057781;
16-OCT-2001
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                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                 Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y. Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohi Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi Masuchi Y., Shizuya H., Kikuchi H.;
                                                                                                        EMBL; AP000001; BAA31940.1; -.
EMBL; AP000007; BAA31940.1; JOINED.
EMBL; AP000007; BAA31943.1; -.
EMBL; AP000001; BAA31943.1; JOINED.
                                                                                                                                                                                                                                                  "Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3."; DNA Res. 5:55-76(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytokine; Glycoprotein;
                                                                 SEQUENCE
                                                                                     Hypothetical
TRANSMEM
                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98344137;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea;
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16-0CT-2001
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SMART; SM00190; IL4_13;
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llarity 100.0%; F
Conservative 0;
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                                                                                               protein; Transmembrane;
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87; Interleukin_13; 1.
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K.,
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Best Local
 RA05_ORYSA
Q01881;
Q1-JUN-1994
Q1-JUN-1994
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CARBOHYD
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lymphotoxin-beta (LT-beta) (Tumor necrosis factor C) (TNF-C)
necrosis factor ligand superfamily member 3) (Fragment).
LTB OR TNFSF3 OR TNFC.
                                                                                                                                                                                                                                                                                                                                                       Prodom; PD002012; TNF_abc; 1
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence of the swine major histocompatibility complex containing all non-classical class I genes.";
Tissue Antigens 57:55-65(2001).
-!- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May prole in immune response regulation. Provides the mem for the attachment of the heterotrimeric complex to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restricted by the company of the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chardon P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Large white; TISSUE=Fibroblast; MEDLINE=21108615; PubMed=11169259;
                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                          Cytokine; Cytotoxin; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00229; TNF;
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InterPro; IPR000478; TNF_family.
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(less prevalent) two LTA and one LTB subunits.
SUBCELLULAR LOCATION: Type II membrane protein (By similarity).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                               GLYYLYC
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                                                     STANDARD;
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                                                       PRT;
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red. No. 32;
Mismatches
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Best Local
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P11457;
01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
H1stone-like protein HLP-1 precursor (DNA-binding HLFA OR SKP OR OMPH OR B0178 OR Z0190 OR ECS0180.

EScherichia coli, and
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Holck A., Kleppe K.;
                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                               Escherichia coli 0157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0808; AMIASEINHBTR.
SMART; SM00499; AAI; 1.
PROSITE; PS00426; CEREAL_TRYP_AMYL_INH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta;
Ehrhartoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seed
                "Cloning and sequencing of Escherichia coli.";
                                                                                              SEQUENCE FROM N.A.,
                                                                                                                                                            Escherichia
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Escherichia
ne 67:117-124
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S31078; S31078.
; P01085; 1HSS.
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allergenic pr
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Pr00234; tryp_alpha_amyl; 1.
S; PR00808; AMLASEINHBTR.
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1 26 POTENTIAL.
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157 /
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Oryzeae; Oryza
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H., Yamada T., T
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                                                                                                                                                                             subdivision;
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a; Poales; Poaceae;
                                the DNA-binding 17K protein
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(C STRAIN=K12 / MG1655;

(C MEDLINE=97426617; PubMed=9278503;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., buare.

RA Riley M., Collado-Viddes J., Glasner J.D., Rode C.K., Mayhew G.F.

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.

RA Mau B., Shao Y.;

RA Mau B., Shao Y.;
CRESTANCE REPARE OF REPARE REP
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STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Rose D.J., Mayhew G.F., Evans P.S., Boutin A., Shao Y., Miller L., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K. Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

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                     constituent?"
FEBS Lett. 26
                                                                                                                                                                                                   SEQUENCE OF 21-32.

STRAIN-K12 / EMG2;

MEDLING-97443975; PubMed-9298646;

Link A.J., Robison K., Church G.M.;

"Comparing the predicted and observed properties in the genome of Escherichia coli K-12.";

Electrophoresis 18:1259-1313(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-0157:H7 / RIMD 050952;

MEDLINE-21156231; PubMed-11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Y
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., T
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Ya
Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia
0157:H7 and genomic comparison with a laboratory strain K-1
DNA Res. 8:11-22(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schramm S., Duncan M.
Davis K., Federspiel
Lashkari D., Lew H.,
                                                                     SIMILARITY TO S. TYPHIMURIUM OMPH.
MEDLINE-90201355; PubMed-2318304;
Hirvas L., Coleman J., Koski P.,
"Bacterial 'histone-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cloning and nucleotide sequence allele from Escherichia coli.";
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MEDLINE=91100302; PubMed=1987124;
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N., Hyman R., K
Lin D., Namath
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R., Kalman S., K
nath A., Oefner
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fner P., Robert
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a R., Ichihara S.,
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M., Tobe T.,
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EMBL; D83536; BAA77853.1; -.
EMBL; U70214; AAB08607.1; -.
EMBL; AE005194; AAG54480.1; -.
EMBL; AE005194; AAG54780.1; -.
EMBL; AF002550; BAB33603.1; -.
EMBL; X54797; CAA38567.1; -.
EMBL; X75465; CAA353207.1; -.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra Saunders D., Shownkeen J.
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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                                                        Nature 368:32-38(1994).
                                                                                                                                                                                                                 STRAIN=Bristol N2;
MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                               Rhabditidae; Pel
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                        Hypothetical
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           European
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$13728; $13728.
ene; EG10455; hlpa.
          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                             Mb of contiguous nucleotide
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation updat)
protein D2007.4 in chromosome
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ilarity 100.0%;
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Caenorhabditis.
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RESULT 24
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Best Local S
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Pfam; PF00061; lipocalin;
PRINTS; PR00179; LIPOCALIN
PROSITE; PS00213; LIPOCALIN
                                                                                                                                          modified and this statement is not removed entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUB=Mammary gland;
MEDLINE=99304500; PubMed=10376212;
MEDLINE=99304500; Nayak S., Apparao K.B.C.,
Das P., Jain S., Nayak S., Apparao K.B.C.,
"Molecular cloning and sequence analysis of
beta-lactoglobulin in Bubalus bubalis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LACE_BUBBU STANDARD; PKI; LACE_BUBBU STANDARD; PKI; P02755; O62822; 21-JUL-1986 (Rel. 01, Created) 15-JUN-2002 (Rel. 41, Last sequence up 15-JUN-2002 (Rel. 41, Last annotation) 15-JUN-2002 (Rel. 41, Last annotation)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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                                               InterPro; IPR002345; Lipocalin.
InterPro; IPR000566; Lipocln_cytrABP
                                                                               PIR; A03219; LGBUI.
HSSP; P02754; 1BSQ.
                                                                                                               EMBL; AJ005429; CAA06532.1;
                                                                                                                                                                                          the European Bioinformatics Institute. Th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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NCBI_TaxID=89462;
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                                                                                                                                                                                                                                                                                                      in milk.
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D2007.4; CE00129.
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LIPOCALIN;

Transport; Lipocalin; Signal.

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RESULT
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CHAIN
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SEQUENCE
      _CAPHI
                                                                                                                             Preaux G., Braunitzer G., Schrank B., Stangl A.;
"The amino acid sequence of goat beta-lactoglobulin.";
"The amino acid sequence of goat beta-lactoglobulin.";
HOPPE-Seyler's Z. Physiol. Chem. 360:1595-1604(1979).

1- FUNCTION: Primary component of whey, it binds retinol and is probably involved in the transport of that molecule.

1- SUBURIT: UNDER PHYSIOLOGICAL CONDITIONS BETA-LACTOGLOBULIN EXISTS AS AN EQUILLBRIUM MIXTURE OF MONOMERIC AND DIMERIC FORMS.

1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                           MEDLINE=95213451; PubMed=7699130;
FOICh J., COll A., Sanchez A.;
"Complete sequence of the caprine beta-lactoglobulin gene.";
J. Dairy Sci. 77:3493-3497(1994).
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Ssp. aegagrus; TISSUE-Mammary MEDLINE-94042559; PubMed-8226387;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Caprinae; Capra.
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
Bovidae; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-MAY-1992 (Rel. 22, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Reta-lactoglobulin precursor (Beta-LG)
                                                                                                                                                                                                                MEDLINE-80070611;
                                                                                                                                                                                                                          SEQUENCE OF 19-180.
                                                                                                                                                                                                                                                                                      TISSUE-Liver
                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   Submitted (JAN-1993)
                                                                                                                                                                                                                                                                                                                              Kim J.,
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                 "Cloning and sequencing of the cDNA lactoglobulin.";
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                                                                                       MISCELLANEOUS: ALTERNATE DISULFIDE BONDS OCC
SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
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Eutheria;
                                                                                                                       SPECIFICITY:
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Mismatches
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EMBL; Z1956; CAA79623.1;
EMBL; Z1956; CAA79624.1;
EMBL; Z33881; CAA83946.1;
PIR; A03320; LGGT.
PIR; S14507; S14507.
PIR; S14507; S42800.
                                        SPECIES-Sheep;
MEDLIND-89057492; PubMed-3194215;
Harris S., Ali S., Anderson S., A
"Complete nucleotide sequence of
                                                                                                                                                                                           J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
CHAIN
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01-AUG-1988 (Rel. 08, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
Beta-lactoglobulin 1/B, 2/A, and 3/C p
Ovis aries (Sheep), and
Ovis orientalis musimon (Mouflon).
                                                                                                                                                                                                       Similarity to the genes secretory proteins.";
J. Mol. Biol. 199:415-42
                                                                                                            "Ovine beta-lactoglobulin messenger RNA: levels during functional differentiation biochimie 68:1097-1107(1986).
                                                                                                                                                                SPECIES=Sheep;
MEDLINE=87049827;
                                                                                                                                                                                                                                                         SPECIES-Sheep; MEDLINE-88172489; PubMed-3351935;
                                                                                                                                                                                                                                                                                               Bovidae; Caprinae;
NCBI_TaxID=9940, 9
                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Cetartiodactyla; Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                        SHEEP
SPECIES=Sheep;
          SEQUENCE FROM
                              Nucleic
                                                                                          SEQUENCE FROM N.A.
                                                                                                                                            Furet J.-P.;
                                                                                                                                                     Gaye P., Hue-Delahaie D., Mercier J.-C.,
                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                 Ali S.,
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (BLG 1 AND
                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                   LACB_SHEEP P02757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Milk; Whey;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00179; LIPOCALIN. PROSITE; PS00213; LIPOCALIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00061; lipocalin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000345; Lipocalin. InterPro; IPR000566; Lipocln_cytFABP.
                                                                                                                                                                                                                                    "Characterization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 LGLALAC
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                              Acids
                                                                                                                                                                                                                                                 Clark A.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.5%;
nilarity 100.0%;
Conservative 0
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         z
                              Res.
                                                                                                                                                                                                       199:415-426(1988).
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                                                                                                                                                                                                                                                                                                   9938;
                                                                                                                                                                PubMed=3096387;
          97a)
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                              16:10379-10380(1988)
                                                                                          (BLG 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19975
                                                nderson S., Arch:
sequence of the
                                                                                                                                                                                                                           gene encoding for retinol bir
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: C2449BB02A1A80F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport; Lipocalin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BETA-LACTOGLOBULIN
                                                                                                                                                                                                                                                                            2)
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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precursor.
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38;
                                                                                                                                                                                                                                    ovine beta-lactoglobulin.
                                                                                                                       nucleotide sequence and mRNA
of the mammary gland.";
                                                                                                                                                      Soulier S.,
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                                                           A.L.,
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                                                  ovine
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                                                            Clark A.J.;
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                                                  beta-lactoglobulin
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                                                                                                                                                       Vilotte J.-L.,
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THE REAL PROPERTY OF THE PROPE
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MEDLINE-89374823; PubMed-2775495;
Erhardt G., Godovac-Zimmermann J., Conti
"Isolation and complete primary sequence
beta-lactoglobulin C.";
beta-1actoglobulin C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWI
between
                                    HSSP; P02754; 1BSQ.
InterPro; IPR002345; Lipocalin.
InterPro; IPR0020566; Lipocln_CytFABP
Pfam; PF00061; lipocalin; 1.
PRINTS; PR00179; LIPOCALIN.
PROSITE; PS00213; LIPOCALIN; 1.
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or send a
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PIR;
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MEDLINE-80219294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preaux G., Braunitzer G., Kolde H.-J.; "Primary structure of ovine beta-lactoglobulin."; Arch. Int. Physiol. Biochim. 88:B45-B46(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88106996; PubMed=3426802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=0.o.musimon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91007276; PubMed=1976573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                A03221; LGSH.
$00132; $00132;
A30011; A30011.
B30011; B30011;
A25136; A25136;
J00748; J00748;
J00749; J00748;
J00749; J00748;
S04955; $04955;
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SUBUNIT: UNDER PHYSIOLOGICAL CONDITIONS BETA-
AS AN EQUILIBRIUM MIXTURE OF MONOMERIC AND DI-
MISCELLANEOUS: ALTERNATE DISULFIDE BONDS OCCU-
SIMILARITY: BELONGS TO THE LIPOCALIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovac-Zimmermann J., Conti A., Napolitano L.; e complete amino-acid sequence of dimeric beta-lactoce control of the mino-acid sequence of dimeric beta-lactoce flon (Ovis ammon musimon) milk.";
1. Chem. Hoppe-Seyler 368:1313-1319(1987).
FUNCTION: LACTOGLOBULIN IS THE PRIMARY COMPONENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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X12817; CAA31305.1;

X07004; CAA30059.1;

X07005; CAA30059.1;

X07006; CAA30059.1;

X07006; CAA30059.1;

X07007; CAA30059.1;

X07008; CAA30059.1;

X07009; CAA30059.1;

X07009; CAA30059.1;

X07009; CAA30059.1;
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                    Whey;
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                  Retinol-binding;
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                  Signal; Lipocalin
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c beta-lactoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BETA-LACTOGLOBULIN EXISTS AND DIMERIC FORMS.
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Best Local S
Matches
                                                                                                                                                                                           Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebalhia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hanlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Complete genome servence" -
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT
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        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb
                                                                                                                                                                    "Complete genome sequence of a multiple enterica serovar Typhi CT18.";
Nature 413:848-852(2001)
                                                                                                                                                                                                                                                                                                                                                                           McClelland M., Sanderson K.E., Spieth J., Cl. Courtney L., Porwollik S., Ali J., Dante M., Leonard S., Nguyen C., Scott K., Holmes A., (Ryan E., Sun H., Florea L., Miller W., Stonel Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhimurium, au
Salmonella typhi.
Bacteria; Proteobacteria;
                                                                 This
                                                                                                                        -i- FUNCTION: May be part of a membrane complex transport (By similarity).
-i- SUBUNIT: Composed of at least six subunits; rnfD, rnfE and rnfG (By similarity).
                                                                                                                                                                                                                                                                                                SPECIES=S.typhi; 9
MEDLINE=21534947;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720; MEDLINE=21534948; PubMed=11677609;
                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella.
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                                         the European Bioinformatics Institute.
                                                       between
                                                                                                               -!- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                             Nature 413:852-856(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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15-JUN-2002 (Rel.
15-JUN-2002 (Rel.
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                                                                                         SIMILARITY: BELONGS
                                                      SWISS-PROT entry is copyright. It is produ
een the Swiss Institute of Bioinformatics
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license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                    of Salmonella enterica
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                                                     produced through a catics and the EMBL
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S., Layman D.
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RX MEDLINE-21156231; PubMed-11258796;
RX Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yoko RA Hayashi T., Tohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasun RA Kuhara S., Shiba T., Hattori M., Shinagawa H.; Tomplete genome sequence of enterchemorrhagic Escherichia col T. Tolf: Tanaka genomic comparison with a laboratory strain K-12. DNA Res. 8:11-22(2001).
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RNFE_ECO57
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                                                           the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glass

Perna N.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpa

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpa

Posfal G., Hackett J., Klink S., Boutin A., Shao Y.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Po

Apodeca J., Anantharaman T.S., Lin J., Yen G., Schwal
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Welch R.A., Blattner F.R.;
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15-JUN-2002
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5-JUN-2002 (Rel. 41, Last sequence update)
5-JUN-2002 (Rel. 41, Last annotation update)
1-lectron transport complex protein rnfE.
NFE OR Z2642 OR ECS2341.
Scherichia coli 0157:H7.
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J1913.
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                                                                                                                                                                        transport (By similarity).
SUBUNIT: Composed of at least six subunits;
rnfD, rnfE and rnfG (By similarity).
SUBCELLULAR LOCATION: Integral membrane pro
                                                                                                                                    (Potential).
SIMILARITY: BELONGS
                                                                             SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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   and this
requires
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POTENTIAL.
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http://www
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rkpatrick H.A.,
Y., Miller L.,
, Potamousis K.,
hwartz D.C.,
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Tobe T.,
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RESULT 29
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Electron
                                                                    "A 570-kb DNA sequence of the Escherichia corresponding to the 28.0-40.1 min region DNA Res. 3:363-377(1996).
                                                                                                Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K
Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mo
Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio
Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S.,
Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
Yamamoto Y., Horluchi T.;
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Saeaef A., Johansson M., Wallin E., von "Divergent evolution of membrane protein coli RnfA and RnfE homologues.";
                                                                                                                                                                                                                                         Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
STRAINE=97426617; PubMed=9278503;
                             STRAIN=K12 / JM109;
MEDLINE=99342054; PubMed=10411911;
                                                                                                                                                                                                                               Gregor J., Davis N.W.,
Mau B., Shao Y.;
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01-NOV-1997 (Rel. 35, Last
15-JUN-2002 (Rel. 41, Last
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01-NOV-1997
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                                                                                                                                                                                                             Science
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                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
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B ALGLGLA
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IPR003667; Rnf_Nq
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CYTOPLASMIC
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D4A2CA2D292604C3 CRC64;
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RRESULT 30
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16-OCT-2001 (Rel. 4
                                                           MEDLINE-95131751; Pubmed-Yosussis, Court D.L.;
Zuber M., Hoover T.A., Powell B.S., Court D.L.;
"Analysis of the rnc locus of Coxiella burnetii.";
MOL. Microbiol. 14:291-300(1994).
-i- FUNCTION: DIGESTS DOUBLE-STRANDED RNA. INVOLVED IN THE PROCESSING OF RIBOSOMAL RNA PRECURSORS AND OF SOME MRNAS (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Coxiella group; Coxiella. NCBI_TaxID=777;
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-!- FUNCTION: May be part of a membrane complex involved in electron transport (By similarity).
-!- SUBUNIT: Composed of at least six subunits; rnfA, rnfB, rnfC, rnfD, rnfE and rnfG (By similarity).
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SIMILARITY: CONTAINS 1 DRBM (DOUBLE-STRANDED RNA-BINDING) DOMAIN
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PROSITE; PS50137; DS_RBD; 1.
PROSITE: PS00517; RNASE 3_1; 1.
PROSITE; PS50142; RNASE_3_2; 1.
   between the Swiss Institute or Lite. The European Bioinformatics Institute. The European Bioinformatics Institutions as long
                           This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsi the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                       -:- SUBUNIT: Composed of at least six subunits;
    rnfD, rnfE and rnfG (By similarity).
-:- SUBCELLULAR LOCATION: Integral membrane pro
                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of Yersinia pestis, the causative agent of plague.";
Nature 413:523-527(2001).
-!- FUNCTION: May be part of a membrane complex involved in electron transport (By similarity).
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Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M. Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M. Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Tarraga M. M., Davies R.M., Davis P., Dougan G., Tarraga M. M., Davies R.M., Davis P., Dougan G., Tarraga M. M., Tarrag
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-!- SIMILARITY: BELONGS TO THE NQRDE/RNFAE FAMILY.
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Churcher C., Mungall K.L.,
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                                                                                                                a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          മ
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Matches 7
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RNFE_HABIN STANDAND,
057020; P96346;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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SEQUENCE
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Pfam; PF02
                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                      EMBL;
TIGR;
                                                                                                                                                                                             -!- FUNCTION: May be part of a membrane complex transport (By similarity).
-!- SUBUNIT: Composed of at least six subunits; rnfD, rnfE and rnfG (By similarity).
-!- SUBCELLULAR LOCATION: Integral membrane prot
                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Ulterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
              Pfam;
                                                                                                                                                                                                                                                                            Rd."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95350630; PubMed-7542800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=727;
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SIMILARITY: BELONGS TO THE
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                                      U32841; AAC23334.1;
HI1688; -.
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              PF02508;
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                         IPR003667; Rnf_Nqr.
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              Rnf-Ngr;
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to license@isb-sib.ch).
  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
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                                                                                                                                                                                                                                                 part of a membrane complex involved
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  Inner
                                                                                                                                                                                                                                                                                     assembly of Haemophilus influenzae
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membrane; Complete proteome
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Best Local :
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or send a
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SEQUENCE
                                                                                                                                                                                                                       "Mouse LIGHT; molecular genetics, ligand binding an Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databer FUNCTION: Cytokine that binds to TMFRSF3/LTBR. decoy receptor TMFRSF6B modulates its effects, and stimulates the proliferation of T cells.
                                                                                                                                                                                                                                                                                                                                                                                                            Tamada K., Shimozaki K., Chapoval A.I., Zhu G., Sica G., F Boone T., Hsu H., Fu Y.-X., Nagata S., Ni J., Chen L.; "Modulation of T-cell-mediated immunity in tumor and graft disease models through the LIGHT co-stimulatory pathway."; Nat. Med. 6:283-289(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002
15-JUN-2002
15-JUN-2002
          EMBL;
EMBL;
HSSP;
                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal liver;
Misawa K., Nosaka T., Kitar
"Murine LIGHT, a homologue
                                           EMBL;
                                                                                                                                                           +
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                                                                                                                                                                                                                                                                                    Force W.R.,
                                                                                                                                                                                                                                                                                             TISSUE-Lymphoma;
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1999)
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=10700230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNFSF14 OR LIGHT
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                                                                                                                                                         proteolytic
SIMILARITY:
                                                                                                                                                                                                     SUBURIT: Homotrimer (F
SUBCELLULAR LOCATION:
                                                                                                                                                                                 PTM: The soluble form
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          AF123385;
AB029155;
AF227533;
P01375; 4T
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                                                                  s requires a license agreement (See http://www.isb-sib
an email to license@isb-sib.ch).
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93
117
152
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Todd P.K., Mikayama T.;
Todd P.K., Mikayama T.;
Todd P.K., Mikayama T.;
Todd P.K., Mikayama T.;
Todd P.K., Mikayama T.;
Todd P.K., Mikayama T.;
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(Rel. 41, Last sequence up
(Rel. 41, Last annotation
sis_factor ligand superfami
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                     AAF76453.1;
BAA88559.1;
AAF36722.1;
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BELONGS TO THE
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Rodentia;
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Pred. No. 47;
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Sciurognathi;
                                                                                                                                                         TUMOR NECROSIS FACTOR FAMILY.
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n LIGHT which is a
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. 47;
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thi; Muridae; Murinae; Mus
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                                                                                                                                                                 This SWI
between
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STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed=10984043;

MEDLINE-20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Lagrou M.

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Golltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Smith K.A., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

Tomplete Geography of Decomposition of Decompo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   opportunistic pathogen.";
Nature 406:959-964(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PSEAE
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                                                                                                                                 the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *Complete genome sequence of Pseudomonas aeruginosa PAO1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003636;
InterPro; IPR000478;
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                                                                                                                                                                                                                                                                                                                                   FUNCTION: May be part of a membrane complex transport (By similarity).
SUBUNIT: Composed of at least six subunits; rnfD, rnfE and rnfG (By similarity).
                                                                                                                                                                                                                                           (Potential).
SIMILARITY: BELONGS TO THE NORDE/RNFAE FAMILY
                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION:
                                                                                                                                                        SWISS-PROT entry is copyright. It is produsen the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SM00207;
non-profit institutions as long as its content is in no way and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 7; Conser
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
angoort complex protein rnfE.
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EXTRACELLULAR (POTENTIAL).
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TUMOR NECROSIS FACTOR LIGAND
MEMBER 14, SOLUBLE FORM.
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01-NOV-1995
15-JUN-2002
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TRANSMEM
                                                                                                                                                                                                                                                                                                          Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D. Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R. Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAEIN
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMed=7542800;
MEDLINE=9535630; PubMed=7542800;
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                                                             TIGR;
                                                                                                or send
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Pfam; PF02508; Rnf-Nqr; 1.
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                         Piam;
                                                InterPro; IPR000205;
                                                                                                                                                                                                                                                                                               "Whole-genome random sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                ACTIVATION OF THE SMALL SUBUNIT OF THE MOLYBDOPTEI FACTOR (MOAD) (BY SIMILARITY).
PATHWAY: MOLYDdenum cofactor biosynthesis.
SIMILARITY: BELONGS TO THE HESA/MOEB/THIF FAMILY.
                                                                                                                                                                                                                                                           ence 269:496-512(1995).
FUNCTION: INVOLVED IN BIOSYNTHESIS
                                                                                                                                                                                                                                    (MOLYBDOPTERIN), NECESSARY FOR MOLYBDOENZYMES. PLAYS A ROLE IN 'ACTIVATION OF THE SMALL SUBUNIT OF THE MOLYBDOPTERIN CONVERTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALGLGLA
                         PF00899; ThiF;
                                                             U32823; AAC23099.1;
HI1449; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE004770; AAG06882.1;
                                                                                               requires a license agreement (See http://www.isb-sib.an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
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                                   IPR000594;
cofactor
243 AA;
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                                  NAD_binding.
ThiF_domain.
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                                                                                                                                                                                                                                                                                                 and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subdivision; Pasteurellaceae;
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48;
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                                                                                                                                                                                                                                                                                                                                                                                                 J.F.
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Molybdenum SEQUENCE

biosynthesis; Complete proteome. 26996 MW; 218A3382A975BDBD CRC64;

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TNFC_HUMAN
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Best Local S
Matches 7
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O1-JUN-1994 (Rel. 29, Created)
O1-JUN-1994 (Rel. 29, Last sequence update)
O1-JUN-1994 (Rel. 29, Last sequence update)
I5-JUN-2002 (Rel. 41, Last annotation update)
Lymphotoxin-beta (LT-beta) (Tumor necrosis factor necrosis factor ligand superfamily member 3).
LTB OR TNFSF3 OR TNFC.
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (ISOFORM 1).

Meville M.J., Milner C.M., Campbell R.D.;

"A new member of the immunoglobulin superfamily subunit are amongst the predicted products of nc TNF locus in the human MHC.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Browning J.L., Ngam-Ek A., Lawton P.,
Chow E.P., Hession C., O'Brine-Greco
"Lymphotoxin beta, a novel member of
heteromeric complex with lymphotoxin
Cell 72:847-856(1993).
                                                       Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
Submitted (DEC-2001) to the EMBL/GenBBR/TNFRSF3. May p
-I- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May p
role in immune response regulation. Provides the mem
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
ROWEN L., Madan A., Qin S., She
Robesi N., Dickhoff R., Loretz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                         -
                                                                                                                                                                            Shiina
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-97445965; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                       Rieder M.J.,
                                                                                                                                SEQUENCE
                                                                                                                                                       Submitted
                                                                                                                                                                   "Homo
                                                                                                                                                                            SEQUENCE F
Shiina S.,
                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                          region."
                                                                                                                                                                                                                                  Lasky S., Hood L.; "Sequence of the human major histocompatibility
                                                                                                                                                                                                                                                                                                          Submitted
                                                                                                                                                                                                                                                                                                                                                                                       Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                        Salles G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93208881;
                                                                                                                                                                                                                                                                                                                                                                                                 lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of two lymphotoxin beta isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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nes 7; Conserv
                     for the attachment of the heterotrimeric complex to the cell surface. Isoform 2 is probably non-functional. SUBUNIT: Heterotrimer of either two LTB and one LTA subunits
  (less prevalent) one LTB and SUBCELLULAR LOCATION: Type II
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                                                                                                                                                                a S., Tamiya
sapiens 2,2
                                                                                                                                FROM
                                                                                                                                                                                       FROM N.A.
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ilarity 100.0%;
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rd N., Charlot C.,
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Commun. 238:273-276(1997).
                                                                                                      Carrington D.P.,
                                                                                                                                                                                      1).
                                                                                                                                                                                                                                                                   Shaffer T., James
                                                                                                                                                     EMBL/GenBank/DDBJ
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                                                                                                                                                        Inoko H.;
omic DNA of 6p21.3 HLA class
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                                                                                                                              AND
                                                                                                                                                                                                                                                          C., Madan
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             two LTA subunits
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the TNF family that forms
on the cell surface.";
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protein
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M., Young
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MCESULT 37

MOEB_ECOLI

ID MOEB_ECOLI

STANDARD;

AC P12282;

DT 01-CCT-1989 (Rel. 12, Created DT 01-CCT-1989 (Rel. 12, Last sen DT 15-JUN-2002 (Rel. 41, Last ann DE MOLYbdopterin biosynthesis provided MOEB OR CHLN OR B0826.

OC Eschill COLI.

OC Bacteria; Provided Coli.
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CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                   194 GLYYLYC
||||||
|31 GLYYLYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01234; TNECROSISFCT ProDom; PD002012; TNF_abc; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; produced by alternative splicing. TISSUE SPECIFICITY: SPLEN AND THYMUS. SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBL
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PS50049; TNF_2; 1.
Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 AA;
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B CYTOPLASMIC
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annotatic
protein m
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DPGAQAQQGL -> GLSAPGSGRT
AAB37342).
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                                 subdivision;
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o. 49;
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                                    Enterobacteriaceae;
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InterPro; IPR000205; i
InterPro; IPR000594; '
Pfam; PF00899; ThiF;
Molybdenum cofactor b
SEQUENCE 249 AA; 20
MOEB_SALTY
Q56067;
Q1-NOV-1997
15-JUN-2002
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MEDLING-97426617; PubMed-9278503;
MEDLING-97426617; PubMedt G. III, Bloch C.A., Perna N.T., Burland V
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Riley M., Collado-Vides J., Glasner J.D., Rode D.J.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                               EMBL; AE000185; AAC73913.1;
EMBL; D90720; BAA35514.1; -
EMBL; D90721; BAA35521.1; -
PIR; B32352; B32352.
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EMBL; AE000185; AAC73913.1
EMBL; D90720; BAA35514.1;
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A 718 kb DNA sequence of the Escherichia corresponding to the 12.7-28.0 min region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nohno T., Kasai Y., Salto T.; "Cloning and sequencing of the Escherichia coli chien operon involved in molybdopterin biosynthesis."; J. Bacteriol. 170:4097-4102(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-88314906; Pu Nohno T., Kasai Y.,
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ROSYNTHESIS OF A DEMOLYBDO COFACTOR

FUNCTION: INVOLVED IN BIOSYNTHESIS OF A DEMOLYBDO COFACTOR

(MOLYBDOPTERIN), NECESSARY FOR MOLYBDOENZYMES. PLAYS A ROLE IN A

ACTIVATION OF THE SMALL SUBUNIT OF THE MOLYBDOPTERIN CONVERTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FACTOR (MOAD).
PATHWAY: Molybdenum cofactor biosynthesis.
SIMILARITY: BELONGS TO THE HESA/MOEB/THIF FAMILY.
                                                                                                                                                          LRYNRQI
                                                                                                                            LRYNRQI
                                                                                                                                                                                         Similarity 7; Conserv
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(Rel.
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Lipopolysaccharide (EC. 2.---)
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modified and this statement is not rem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wong K.K., Kwan H.S. Submitted (APR-1996)
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MEDLINE-21534948; PubMed-11677609;
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Bacteria; Proteobacteria;
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Mulvaney E.,
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(99JM10; Q9JM11;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel.
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Serratia.
                                                                                                                                                                                                                                                                                   Gene 242:295-305(2000).
-i- FUNCTION: Cytokine that binds to LTBR/TNFRSF3. May play a specific
                                                                                                                                                                                                                                                                                                                                        Li D.H., Havell E.A., Brown C.L., Cullen J.M.; "Woodchuck lymphotoxin-alpha, -beta and tumor necrosis structure, characterization and biological activity."; Gene 242:295-305(2000).
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Pfam; PF00535; Glycos_transf_2; 1.

Lipppolysaccharide biosynthesis; Transferase; Glycosyltransferase.

SEQUENCE 257 AA; 29233 MW; D40D7B57E002F990 CRC64;
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MEDLINE-96422003; PubMed-8824620;
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                                                                                  SUBUNIT: Heterotrimer of either two LTB and one LTA subunits of (less prevalent) two LTA and one LTB subunits (By similarity).

SUBCELLULAR LOCATION: Type II membrane protein (Potential).

SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
  European
                                                                                                                                                                                                                                                     role in immune response regulation. Provi for the attachment of the heterotrimeric
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                    SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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Bioinformatics Institute.
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CONFLICT
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HSSP;
194 GLYYLYC
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181 GLYYLYC
                                                                                                                                                                             PRINTS; PR01234; TNECROSISFCT.
ProDom; PD002012; TNF_abc; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                            InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                  SEQUENCE
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                                        7; Conserv
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272
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 187
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32644 MW;
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48
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N-LINKED (GLCNAC. . .) (POTEN

D -> H (IN REF. 1; AAF34865).
                                                   Score 7;
Pred. No.
                                                                                                                                  nbrane; Glycoprotein; Signal-anchor.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                          Mismatches
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. 60;
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Job time Search completed: March 31, 30 secs 2003, 14:14:17

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Total number of hits satisfying chosen parameters:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	5	4	ω	N	1	Result No.
8	8	8	8	8	80	80	8	80	80	8	80	89	80	9	10	Score
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Q9bpv2 homo sapien	Q99908 homo sapien	058554 pyrococcus	Q8szb8 drosophila	Q9cpr8 mus musculu	Q9d378 mus musculu	Q9zg99 pseudomonas	Q8sxh4 drosophila	Q9buil homo sapien	Q9wyu0 thermotoga	Q9vv70 drosophila	Q9sdil oryza sativ	Q9hst7 halobacteri	Q9bx52 homo sapien	Q98ij0 rhizobium l	Q8x4j8 escherichia	Description

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ALIGNMENTS

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RESULT
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DJ831C21.1 (Novel protein similar to gamma-glutamyl
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  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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EMBL; AE005458; AAG57389.1; -.
InterPro; IPR000620; DUF6.
Pfam; PF00892; DUF6; 1.
Hypothetical protein; Complete proteome SEQUENCE 111 AA; 12165 MW; 7CEFC93E
Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                            Q9BX52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamot Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T. Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
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                                                                                               рл831C21.1.
                                                                                                                  transpeptidase-related
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Bacteria; Proteobacteria; alpha
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nilarity 100.0%;
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                                                                                                                  ein similar to gamma-glutamyl protein (GGT-Rel)) (Fragment).
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Last sequence update)
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Y MEDLINE-20504483; PubMed-11016950;

X MEDLINE-20504483; PubMed-11016950; PubMedian M., Norgan M., N
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Best Local
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
""" orthetical protein (OSJNBA0036E02.6 protein) (B10
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Q9HST7;
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                                                   Oryza sativa (Rice).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
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SEQUENCE FROM N.A.
COrby N.;
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Archaea; Euryarchaeota; Halobacteria;
Halobacteriaceae; Halobacterium.
SEQUENCE FROM N.A
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Barndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Baldwin D.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Ge Pablos B., Delcher A., Bownes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Gersell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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01-MAY-2000
01-JUN-2002
CG13033 proto
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Pterygota; Neoptera; Endopte
Ephydroidea; Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JAN-2001) to the EMBL; AP000815; BAA87834.1; EMBL; AP002862; BAB17732.1; EMBL; AP003103; BAB44106.1;
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Eukaryota; Metazoa; Arthropoda; Trac
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Sasaki T., Matsumoto T.,
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"Oryza sativa nipponbare(GA3) genomic
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(TremBLrel. 21, Last ann
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Endopterygota; Diptera; Brachycera; Muscomorpha;
illdae; Drosophila.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
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15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Sylirs B.C., Syradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yeng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
BMEL, ARD03527; AAR49452.1; -.
BREIL; ARD03527; AAR49452.1; -.
BREIL; ARD03527; ALF49452.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

CSTRAIN-MSB8 / DSM 3109;

CSTRAIN-MSB8 / DSM 3109;

XM MEDLINE-99287316; PubMed=10360571;

XM Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

XM Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

XM AM CDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

XM Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson M.D.,

XM Stewart A.M., Cotton M.D., Pratt M.D., Phillips C.A., Richardson M.D.,

XM Stewart A.M., Cotton M.D., Pratt M.D.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Thermotogae; NCBI_TaxID=2336;
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                                                                           SLLDFEIS
SLLDFEIS
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8; Conserv
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8; Conser
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197 AA; 2
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                                                                                                                                                                                                                                                                                                                  n; Complete proteome.
22919 MW; 41E2C8E3C09180EC CRC64;
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                                                                                                                                                                                                Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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18;
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19;
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                                                                                                                                                                                                                                          Length 197;
                                                                                                                                                               Indels
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RESULT 8 Q9BUI1 ID Q9BU

Q9BUI1

PRELIMINARY;

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RESULT
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ID Q9
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01-JUN-2001 (TrEMBLrel. 17, Creat
01-JUN-2001 (TrEMBLrel. 17, Last
01-JUN-2002 (TrEMBLrel. 21, Last
1 Hypothetical 22.8 kDa protein.
3 Homo sapiens (Human).
5 Eukaryota; Metazoa; Chordata; Cr
                              Q9ZG99
Q9ZG99;
Q9ZG99;
Q1-MAY-1999 (TrEMBLrel. 1
01-MAY-1999 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8SXH4
Q8SXH4;
Q1-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
  Transmembrane pampe or PA4521
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AY089634; AAL90372.1; -. SEQUENCE 211 AA; 23780 MW; 82FF4983E91F510A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Mectazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Celniker S.;
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BC002598; AAH02598.1; -
Pro; IPR004299; MBOAT_fam.
Pr03062; MBOAT; 1.
                                                                                                                                                                                                                                                                                                                                  Similarity
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(TrEMBLrel.
(TrEMBLrel.
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                                                                                                                                                                                                                                                                 79
                 protein
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                                                                                                                                                                                                                                                                                                                                                                                            23780 MW;
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1. 10,
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AMPE.
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                                                                                                                                                                                                                                                                                                          Score 8; DB 5; Pred. No. 21; 0; Mismatches
                                      Last sequence up
                                                                             Created)
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RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Q9D378;
Q9D378;
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "An ampD gene in Pseudomonas aeruginosa of ampC beta-lactamase expression."; Submitted (AUG-1998) to the EMBL/GenBank
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=C57BL/60; TISSUE=MEDULLA OBLONGATA;
MEDLINE=21085650; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AF082575; AAC98784 1; -.
EMBL; AE004866; AAG077909.1; -.
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STRAIN-ATCC 15692 /
MEDLINE-20437337; Pu
Wynshaw-Boris A.,
Hayashizaki Y.;
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STRAIN-ATCC 15692 /
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Insecta;

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Airawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Built C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Built C., Fletcher C., Fujita M., Gariboldi M.,
RA Blake J., Built C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
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                                                                                                                                                                                                                 Auquier P.H., Chomez P.M., De Backer O.R., Bertrand "Ten new murine members of the MAGE gene family."; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databa EMBL; AK017727; BAB30899.1; -. EMBL; AK010294; BAB26830.1; -. EMBL; AK010294; BAB26830.1; -. EMBL; AF319979; AAK01207.1; -. EMBL; AF319979; AAK01207.1; -.
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EMBL; AK018250; BAB31133.1; -.
MGD; MGI:1913897; 5730494G16R1k.
InterPro; IPR002190; MAGE.
Pfam; PF01454; MAGE; 1.
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MEDLINE=21085660; PubMed=11217851;
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Mammalia; Eutheria;
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5730494G16R1k protein (Mage-g1).
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                                                                                                        Length 279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2002
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                   Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Naga Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguc Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1998 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY070982; AAL48604.1; -. SEQUENCE 306 AA; 34083 MW; 32B69371475A48F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; He
Eterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                   Hypothetical SEQUENCE 3:
                                                                                                      Pfam; PF01758; SBF; 1.
                                                                                                                                                                                         "Complete sequence and gene organization thermophilic archaebacterium, Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pyrococcus horikoshii.
Archaea; Euryarchaeota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea; Dro
NCBI_TaxID=7227;
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                                                                                                                      EMBL; AP000003; BAA29917.1; InterPro; IPR002657; BileAc,
                                                                                                                                                                         DNA Res. 5:55-76(1998
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PH0824.
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                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98344137;
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                                                                   al protein; Complete 339 AA; 37228 MW;
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                     PubMed=9679194;
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34083 MW;
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rel. 09,
rel. 20,
rel. 20,
  2.8%;
                                                                                                                               BileAc/Na_smprtr.
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  Score 8;
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E91697D5C8C3705F CRC64;
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annotation update)
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Thermococcales; Thermococcaceae;

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DB 17;

Length 339;

of the genome of a horikoshii OT3.";

Nagai Y., 0guch1

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RESULT 16
Q9BPV2
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InterPro; 1.
"Fam; PF03062; Mbc.
"Fam; A2 AA;
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01-MAY-1997 (
01-MAY-1997 (
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9BPV2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Unknown (protein for MGC:4221) (protein for MGC:2099).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-KIDNEY, AND COLON;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-96273128; PubMed-8702217;
Fukunaga-Johnson N., Lee S.W., Liebert M.,
"Molecular analysis of a gene, BB1, overex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Homo sapiens (Human).
Thervota; Metazoa; Chordata; (
                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anticancer Res. 16:1085-1090(1996).
EMBL; S82470; AAB37433.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oreast carcinoma.
                                                       311
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                                                       ALGLGLAL
                                                                                                  ALGLGLAL
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                                                                                                                                                                                                                                            PF03062;
NCE 343
                                                                                                                                                                                                                                                                                   tted (FEB-2001) to the EMBL/GenBank/DDBJ databases BC003164; AAH03164.1; -. BC002512; AAH02512.1; -. Pro; IPR004299; MBOAT_fam.
                                                                                                                                                Similarity
8; Conser
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7 (TrEMBLrel.
2 (TrEMBLrel.
                                                                                                                                                Conservative
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                                                                                                                                                                                                                                            AΑ;
                                                                                                                                                                                                                                                                    MBOAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                            38727 MW;
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Last annotation updat
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                                                                                                                                                                                            Score
                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Ve Catarrhini;
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                                                                                                                                                                                                                                            F71E7DBF74BD9BB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2B479EA8CFF1B91C CRC64;
                                                                                                                                              Mismatches
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overexpressed in bladder
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                                                                                                                                                        DB 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                            Length 343;
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                                                                                                                                                Indels
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                                                                                                                                           Gaps
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STRAIN-AV19 / DSM 6324 / JCM 9639;
STRAIN-AV19 / DSM 6324 / JCM 9639;
STRAIN-AV19 / DSM 6324 / JCM 9639;
Sheherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Sheherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Sheherbinina O.V., Shakhova V.V., Belova G.I., Aravind L., Shakhova V.V., Belova G.I., Aravind L., Sheherbinina O.V., Kozyavkin S.A.;
Matale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stette Malykh A.G., Koonin E.V., Kozyavkin S.A.;
"The complete genome of hyperthermophile Methanopyrus kand and monophyly of archaeal methanogens.";
Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
EMBL; AE010455; AAM02868.1; -.
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EMBL; AE010455; AAMO
Complete proteome.
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Q8TUU8;
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                            MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eighmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacteriam tuberculosis.

Mycobacteriam firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacteria; Mycobacteriaceae; Mycobacter
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01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
Hypothetical protein cysm3
                                             TubercuList; Rv0848; InterPro; IPR001926; Pfam; PF00291; PALP;
  Hypothetical SEQUENCE 37
                                                                                                                   EMBL; AL022004; CAA17654.1;
HSSP; P35520; LJBQ.
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NCBI_TaxID=1773;
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NCBI_TaxID=2320;
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n; Complete proteome.
40118 MW; 927386BE1DF5FB6C CRC64;
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O9KYT3;
O1-OCT-2000 (TrEMBLrel. 15, Creater,
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update,
O1-OCT-2000 (TrEMBLrel. 21, Last annotation update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative integral membrane protein.
SCO5682 OR SC5H4.06C.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
---innmycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Q9SHD8;
Q1-NAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
At2g45000 protein (At2g45000/T14P1.20) (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quall M.A., Kieser H.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
STRAIN-CV. COLUMBIA; MEDLINE-20083487; PubMed-10617197; MEDLINE-20083487; PubMed-10617197; Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffa Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gil
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence coelicolor A3(2).";
Nature 417:141-147(2002).
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VCE 377 AA; 37614 M
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eudicots; Rosid
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Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo I Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan
                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 11 01-JUN-2002 (TrEMBLrel. 21, 11 Hypothetical protein Atu3948 ATU3948 OR AGR_L_1808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Arabidopsis Full Length cDNA Clones."; Submitted (FEB-2002) to the EMBL/GenBan EMBL; AC007659; AAD32835.1; -. EMBL; AY074646; AAL69462.1; -. EMBL; AY080620; AAL86303.1; -.
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                                                                                                              SEQUENCE FROM N.A. MEDLINE=21608550; PubMed=11743193;
                                                                                                                                                                      Bacteria; Proteobacteria; Rhizobiaceae; Rhizobium.
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Submitted (JAN-2002) to the
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STRAIN=CV. COLUMBIA;
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Q8XS70;
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                                                                                                                  PROSITE;
Plasmid;
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EMBL; AE008289; AAK89478.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 397 AA; 41708 MW; 700748E32A46AE86 CRC64;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=305;
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358
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Mismatches
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01-MAY-2000
01-MAY-2000
Burtis K.C., Busam D.A., Butler H., Cadieu E., Cénter A., Chandra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunrobin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum H., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
                                                                                                                                                                            Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Bucka D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Chandra I., Burtie K., Bucka D., Butchan M.R., Bouck J., Brokstein P., Brottler P., Chandra I.
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01-MAR-2002 (TrEMBLrel. 20, La
Hypothetical 47.4 kDa protein.
DKFZP5660011.
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Submitted (SEP-1999) to the
EMBL; AL117414; CAB55910.1;
MEROPS; T03.002;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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pRINTS; PR01210; GGTRANSPTASE.
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shide B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

RA Zheng S.R.J., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

EMBL, AEOU360; AAF51889 1; -

DR Flybase; FBgn0037428; CG1169.

SEQUENCE 454 AA; 51320 MW; A75AAAD97E716573 CRC64;
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MEDLINE-21470413; PubMed-11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebalhia M., James K.D., Churcher C., Mungall K.L.,

Prentice M.B., Sebalhia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
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01-MAR-2002
01-JUN-2002
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                                                                                                                                                                                                                                                                                  Interpro; IPR003662; sub_transporter.
Pfam; PF00083; sugar_tr; 1.
Hypothetical protein; Complete proteor
SEQUENCE 465 AA; 50176 MW; 0CC2731
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                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of Yersinia Nature 413:523-527(2001).
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01-MAY-2000
01-MAY-2000
01-MAR-2001
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last sanotation update)
01-JUN-2002 (TrEMBLrel. 21, Last sanotation update)
CDNA FLJ31346 fits, Clone MESAN1000180, highly similar to
cell expression-enhanced gene/tumor progression-enhanced
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                                                                                                                         Pfam; PF(
SEQUENCE
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                                                                                                                                                                                                                     Submitted (OCT-2001) to the EMBL; AK055908; BAB71043.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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EMBL; AE002079; AAF12043.1; -.
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100.0%;
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16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 8;
                             Score 8; pred. No
                                                                                                                                                                                                                                                project.";
EMBL/GenBank/DDBJ
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Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96B2BEBF6E445D27 CRC64;
                                                                                                                         EA721998043F9EBD CRC64;
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Mismatches
   Mismatches
                                NO.
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42;
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42;
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   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rdson D.L.,
Shen M.,
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RESULT
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Q9CY76
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Keishi M., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Bownstein M., Bulta C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Kayashi H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y., Storch K., F.,
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9CY76;
                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, RIKEN GDNA 573589L02 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-1121/851;
Submitted (FEB-2002)
                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                  Strausberg
                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                     Q8R1P9;
                                                                                                                                                                                                                                          Q8R1P9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse Nature 409:685-690(2001).
EMBL; AK019981; BAB31950.1; -.
MGD; MGI:1924832; 5730589L02Rik.
                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
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                                  EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pro; IPR004299; MBOAT_fam.
PF03062; MBOAT; 1.
NCE 473 AA; 53504 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                        Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
6
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the
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17,
21,
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EMBL/GenBank/DDBJ databases
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Last annotation updat
                                                                                                                                                            Created)
Last sequence up
Last annotation
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 8; I
                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CE6F8E93C3D01C4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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5. 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 473;
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; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Storch K.-F.,
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RESULT
Q9LIW0
   DACE OF THE PROPERTY OF THE PR
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Best Local S
Matches 8
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Best Local S
Matches 8
                                                                                                                                                 J. VIIO1. 73:1146-1155(1999).

-I- FUNCTION: HEWAGGLUTININ IS RESPONSIBLE FOR ATTACHING THE VICELL RECEPTORS AND FOR INITIATING INFECTION (BY SIMILARITY).

-I- SUBUNIT: HOMOTRIMER. EACH OF THE MONOMERS IS FORMED BY TWO (HA1 AND HA2) LINKED BY A DISULFIDE BOND (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. Hsing Y.C., Chow T., Chen C., Wu H., Chu M., Chen Y.C., Chow T., Chen C., Wu H., Chu M., Chen Y.C., Chen Y.C., Wu H., Chu M., Chen Y.C., Chen Y.C., Wu H., Chu M., Chen Y.C., Wu H., Chu M., Chen Y.C., Wu H., Chu M., Chu 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9LIW0;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9LIW0
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SEQUENCE 473 AA; 53382 MW;
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-A/DUCK/POTSDAM/2216-4/84;
MEDLINE-99099002; PubMed-9882316;
Matrosovich M., Zhou N., Kawaoka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza A viruses.
NCBI_TaxID=11320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1999
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
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                                                       -1- SIMILARITY: BELONGS TO EMBL; AF082041; AAD13573.1; HSSP; P03437; 1HTM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9YTU9
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                                                                                                                                                                                                                                                                                                   properties.";
                                                                                                                                                                                                                                                                                                                                        humans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hemagglutinin H5
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                                  nterPro;
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hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31
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wes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                 chickens,
   is); in...
ipR001364; Hemagglutn.
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                 Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Branchennard N.J., Clark L.N., Harris B.R., Melville S., Law Gerrard C., Rajandream M.A., Barrell B.G.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AL359782; CAB95571.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang L.J., Shortridge K.F.;
Zhang L.J., Shortridge K.F.;
"H5N1 Influenza Viruses Isolated f
Fuidence for Genetic Reassortment
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                                                                                             SEQUENCE FROM N.A. STRAIN-TREU927; Hall N., Bowman S.
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MEDLINE-21874832; PubMed-11878904;
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                                                                         Bray-Allen
Lawson D.,
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Best Local :
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Best Local
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Possibly hypothetical protein 85.6 KD.
CHR1.139.
NON_TER
SEQUENCE
                                                                                                                                                                                          J. EXP. ZOOL. 0:0-0(2001).

-i- FUNCTION: PROTAMIES SUBSTITUTE FOR HISTONES IN TH
-i- FUNCTION: PROTAMIES SUBSTITUTE FOR HISTONES IN TH
-i- SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS.

SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INAC-
-i- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hall N., Bowman S., Quail M., Ivens A.C
Lennard N.J., Clark L.N., Harris B.R.,
Gerrard C., Rajandream M.A., Barrell B.
Submitted (JUN-2000) to the EMBL/GenBan
EMBL; AL359782; CAB95435.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
Sperm protamine P3 (Po3) (Fragment).
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01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                             Chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                Gimenez-Bonafe P.,
Ausio J., Kasinsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Mol
Incirrata; Octopodidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=TREU927;
Hall N., Bowman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma brucei.
Eukaryota; Euglenozoa;
                                                        DOMAIN
                                                                               DNA condensation;
                                                                                                                                                                                                                                                                                                                                        vulgaris (Cephalopoda)
                                                                                                                                                                                                                                                                                                                                                    "Chromatin remodelling and protamines vulgaris (Cephalopoda).":
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-SPERM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Octopus vulgaris (Octopus)
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                                                                                                                                     UE SPECIFICITY: TESTIS.
SPECTROMETRY: MW-4389; METHOD-ELECTROSPRAY
  24
                                                                                                          protein; Nucleosome core;
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H.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Octopus
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Chiva M.;
                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation updat
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Pred. No
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                                                        POLY-ARG
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Melville
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                                                                                                             DNA-binding;
                                                                                                                                                                                                                             COMPLEX.
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Best Local S
Matches 7
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Best Local Similarity
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01-MAR-2002 (TrEMBLrel. 20
01-MAR-2002 (TrEMBLrel. 20
01-MAR-2002 (TrEMBLrel. 20
Sperm protamine P5 (Po5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. EXP. ZOOI. 0:0-0(2001).

1: FUNCTION: PROTAMINES SUBSTITUTE FOR HISTONES IN THE CHR SPERM DURING THE HAPLOID PHASE OF SPERMATOGENESIS. THEY SPERM DNA INTO A HIGHLY CONDENSED, STABLE AND INACTIVE IS SUBCELLULAR LOCATION: NUCLEAR.

1: SUBCELLULAR LOCATION: NUCLEAR.

1: MASS SPECTROMETRY: MW=9941; METHOD=ELECTROSPRAY.
Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-DNA condensation; Nuclear protein.

DNA condensation; Nuclear protein.
                                                                                                                                                                            SEQUENCE FROM N.A.
D'Andrea M., Pilla
                                                                                       Submitted
                                                                                                                                                                                                                                                                Bovidae; Caprinae;
NCBI_TaxID=9925;
                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 101-DEC-2001 (TrEMBLrel. 19, 101-DEC-2001 (TrEMBLrel. 19, 101-DEC-2001) precursor BETA-LACTOGLOBULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gimenez-Bonafe P., Ribes
Ausio J., Kasinsky H.E.,
                                                            EMBL; AJ292058;
                                                                                                                  "A new polymorphism region.";
                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                                                                                                                   Capra hircus (Goat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9BEF6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Octopus vulgaris (Octopus).
Eukaryota; Metazoa; Mollusca;
Incirrata; Octopodidae; Octopu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9BEF6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vulgaris (Cephalopoda)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Chromatin remodelling and protamines wildaris (Cephalopoda).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-6645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FISSUE-SPERM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE, FUNCTION,
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                                                                                             (JAN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49
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                                                            2001) to the CAC27455.1;
                                                                                                                                                mF;
                                                                                                                                                                                                                                                                                              Capra.
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Chiva M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
r (Fragment).
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Last sequence up
                                                                                                                                       .ano M.;
beta-lactoglobulin proximal
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Pred. No. 35;
0; Mismatches
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                                                                                       EMBL/GenBank/DDBJ
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14F1BC7E4D277049
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35;
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                                                                                       databases
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                                                                                                                                             promoter
                                                                                                                                                                                                                                                                                                                             Bovoidea;
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RESULT
Q9ZG35
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Query Match
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Best Local
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                                    Usuki K., Gonez L.J., Wernstedt C., Moren A. Claesson-Welsh L., Heldin C.H.;
"Structural properties of 3.0 kb and 3.2 kb platelet-derived endothelial cell growth fac phosphorylase in A431 cells.";
Biochim. Biophys. Acta 1222:411-414(1994).
EMBL; S72487; AAD14107.1;
SEQUENCE 54 AA; 5808 MW; 827925FBA70CB22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09ZG35;
09ZG35;
01-MAY-1999
01-MAY-1999
01-MAY-1999
                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-94312438; PubMed-8038210;
MEDLINE-94312438; PubMed-8038210;
                                                                                                                                                                                                                            Q16193;
Q16193;
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SEQUENCE
                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
Orf2 5' to PD-ECGF/TP protein.
                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chlamydia trachomatis.
Bacteria; Chlamydiales;
NCBI_TaxID=813;
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01-MAY-1999 (TrEMBLrel. 10, 1
01-MAY-1999 (TrEMBLrel. 10, 1
Hypothetical 3.5 kDa protein
                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-1998) to the EMBL; AF087333; AAD04107.1;
                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing."
                                                                                                                                                                                                                                                                                                                                                                                                                               Wang L., Steenburg S. "Gene identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-L2 434B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                      174 NSSSPLR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 LGLALAC
|||||||
8 LGLALAC
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           Similarity
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                                                                                                                                                                                                                                                                                                                                                                 35 AA;
  Conservative
                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                          Conservative
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3372 MW;
                                                                                                                                                                                                                                                                                                                                                               3519 MW;
                                                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                    2.5%;
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                .D., Zheng Y., Larsen S.H of Chlamydia trachomatis
           100.0%;
                     2.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
n (Fragment).
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Pred.
                    Score
                                       827925FBA70CB222
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           Pred. No.
                                                                                                                                                          Catarrhini;
                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                     Pred. No.
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 Mismatches
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                                                                            kb transcripts e factor/thymidine
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                                                                                                         A., Miyazono
                                                                                                                                                          Hominidae;
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                                                                                      transcripts encoding
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                                       CRC64;
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                    Length 54;
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RESULT 40
088028
ID 0880S
AC 08RQS
DT 01-JU
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Search completed: March 31, 2003, 14:15:52 Job time: 88 secs
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                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.5%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 72; Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Baba M., Midorikawa Y., Nakagawa Y., Fujita M., Matsuyama T.;

Baba M., Midorikawa Y., Nakagawa Y., Fujita M., Matsuyama T.;

"Serratia marcescens and Escherichia coli genes controlling

temperature-dependent production of structurally unrelated secondary

metabolites such as prodigiosin and serrawettin.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AB080601; Bab89553.1; -.

Hypothetical protein;

Hypothetical protein;

SEQUENCE 67 AA; 7791 MW; 47B01A87E69AC2A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8RQS4 PRELIMINARY; PRT; 67 AA.
Q8RQS4;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 7.8 kDa protein.
THCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serratia marcescens.

Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Serratia.
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||||||
17 RPRRSAP 23
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[1]
                                                                                                                                                                             55 LLVPLAL 61
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21 LLVPLAL 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 67;
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1444
1 MSLLDFEISARRLPLPRSLG.....PWAHLKAAPFLTYFGLFQVH 284
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                        // SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980 DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	DΒ	ID	Description
	1444	100.0	284	19	AAW47525	Homo sapiens tumou
2	1268	87.8	249	20	AAY09369	Human tumour necro
ω	1268	87.8	249	21	AAB07526	Amino acid sequenc
4	1268	87.8	249	21	AAY95338	Human PRO207 antit
ر. ن	1268	87.8	249	23	AAU86129	Human PRO207 polyp
6	1265	87.6	249	19	AAW29745	TNF related endoth
7	1265	87.6	249	22	AAE00891	Human TREPA (TNF r
8	1066	73.8	273	22	AAU03499	TWEAK extracellula
9	1062	73.5	208	20	AAW93590	Human TNRL3 protei
10	1020	70.6	225	19	AAW47524	Mus musculus tumou

5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
93.5	94	94.5	95	95	95	95	95	95	96	96.5	96.5	99	99	99	100	100.5	102	104	104	104.5	105.5	106	106.5	106.5	106.5	108.5	108.5	116	116	761	792	792	968	1020
										6.7	٠	٠		6.9		٠		7.2	7.2			7.3				7.5			8.0	52.7	4.	54.8	.7	70.6
409	876	1006	294	294	294	294	294	240	234	1631	1097	1020	1008	574	220	647	256	1323	409	779	406	1428	254	254	254	260	211	409	325	146	189	189	211	225
22	22	22	22	22	22	19	19	23	22	22	22	22	22	21	22	17	22	15	23	23	23	21	23	18	16	21	21	23	22	22	22	19	20	21
AAO00076	ABG00217	ABG21178	AAE01992	AAE04425	AAE08737	AAW68292	AAW69956	AAE13680	AAB62339	ABG22481	ABG25655	AAM79875	AAM78891	AAY97032	AAB62340	AAW04327	AAM25657	AAR55248	AAU77716	ABB07845	AAU77717	AAY97033	ABB75953	AAW26657	AAR64190	AAY58215	AAY58216	AAU77718	ABB67553	AAE00895	AAE00892	AAW29746	AAW93591	AAB07527
Human polypeptide	Novel human diagno	Novel human diagno	RANKL (r	Murine receptor ac	Murine receptor ac	NF-kB receptor act	NF-kB receptor act		Gp120 V3 loop-CD15		Novel human diagno	Human protein SEQ	Human protein SEQ	Caspase 8-interact	ש	Rat petrin. Rattu	Human protein sequ	N-methyl-D-asparti	Drosophila melanog	Human MAP kinase p	Drosophila melanog	Caspase 8-interact	Human cytokine 4-1	Human 4-1BB ligand	Human 4-1BB-L poly		Canine mature CD15	Drosophila melanog	elano	Human TREPA (TNF r	മ	elated	TNRL3	Amino acid sequenc

ALIGNMENTS

DR XX	XX	PA	PΑ	XX	PR	PR	PR	XX	ΡF	XX	рD	×	PN	XX	SO	××	ΚW	ΚW	Κ¥	XX	DE .	×	DΤ	XX	AC	××	ID	RESULT 1 AAW47525
### Browning JL, Chicheportiche x; WPI; 1998-145619/13. N-PSDB; AAV18600.	25.	(UYGE-) UNIV GENEVA FACULTY MEDICINE.	(BIOJ) BIOGEN INC.				18-MAR-1997; 97US-0040820.		07-AUG-1997; 97WO-US13945.		12-FEB-1998.		WO9805783-A1.		Homo sapiens.		graft rejection.	cancer; autoimmune disease; immune system; stimulation; suppression;	TRELL; tumour necrosis factor related ligand; tnf; treatment;		Homo sapiens tumour necrosis factor related ligand (TRELL).		21-JUL-1998 (first entry)		AAW47525;		AAW47525 standard; Protein; 284 AA.	LT 1 7525

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RESULT 2
AAY09369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of human tumour necrosis factor related CC ligand (TRELL). TRELL or active fragments can be included with a CC carrier in pharmaceutical compositions to treat cancer, autoimmune CC diseases or immune responses to tissue grafts, or to stimulate or CC suppress the immune system. It is useful to screen for TRELL receptors by labelling with a detectable label and screening CC compositions for binding. Agents interfering with TRELL-receptor CC binding can also be screened for, can then be administered, Optionally with interferon gamma, to induce cell death or CC treat, suppress or alter immune responses (especially involving human CC adenocarcinoma cells) involving a signal pathway between TRELL and its receptor. It's coding sequence can be used in gene therapy for CC TRELL-related disorders in mammals (especially humans), e.g. tumours, CC autoimmune and inflammatory diseases or inherited genetic disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by introducing into cells, and expressing, therapeutically effective amounts of a vector, e.g. a virus comprising a gene encoding TRELL. It may also be of use in the preparation of prepare probes for screening natural/synthetic DNAs for TRELL-encoding sequences
                                                                                                                                NF-kappaB-dependent
                                                                                                                                               Human;
                                                                                                                                                                                                                                                 AAY09369;
                                                                                                                                                                                                                                                                              AAY09369 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                 22-APR-1999
                                                                              Homo sapiens
                                                                                                                cancer.
                                                                                                                                                                                  Human
                                                                                                                                                                                                                15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tumour necrosis factor related ligand - useful for, e.g. treating cancer, auto-immune disease and immune responses to tissue grafts
                                                                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSLLDFEISARRLPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLA
                                                                                                                                                                                                                                                                                                                                                           VNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         \tt LGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGLGLACACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSLLDFEISARRLPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLA
                                                                                                                                                                                tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Pages 50-51;
                                                                                                                           tumour necrosis factor; Apo-3 ligand; lymphotoxin; apoptosis;
pab-dependent transcription; JNK/SAPK-dependent response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0
nilarity 100.0
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              284 AA;
                                                                                                                                                                                necrosis
                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy.
                                                                                                                                                                                                                                                                                Protein;
                                                                                                                                                                              factor
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                                                                                                                                                                                                                                                                              249 AA
                                                                                                                                                                            Apo-3 ligand protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1444; DB 19;
Pred. No. 1.2e-129;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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RESULT 3
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Best Local S
Matches 249
                                                                                                                     TWEAK protein; im
TWEAK blocking ago
Graft-versus-Host
         15-JAN-1999;
                               14-JAN-2000; 2000WO-US01044
                                                                          WO200042073-A1
                                                                                              Homo sapiens.
                                                                                                                                                                 Amino acid
                                                                                                                                                                                                            AAB07526;
                                                                                                                                                                                                                                AAB07526 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic activity. Apo-3 ligand can be used to induce apoptosis in mammalian cancer cells, to induce NF-kappaB-dependent transcription to induce JNK/SAPK-dependent responses in mammalian cells.
                                                                                                                                                                                      20-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a human tumour necrosis factor (TNF) and lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has
                                                     20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human Apo-3 ligand (a tumour necrosis factor) homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX56000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-287982/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1997;
10-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAARRSQRRRGERGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL
                                                                                                                                                                                                                                                                                                                                             LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL
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                                                                                                                                                                                                                                                                                      TYFGLFQVH
                                                                                                                                                                                                                                                                                                          TYFGLFQVH 284
                                                                                                                                                                                                                                                                                                                                                                            GAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD
                                                                                                                                                                                                                                                                                                                                                                                                                      VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                  VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 155
                                                                                                                                                                                                                                                                                                                                  LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL
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249; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑJ,
                                                                                                                                                                sequence of a soluble recombinant human TWEAK protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                    (first entry)
                                                                                                                             immunological disorder; immune response; inflammation; agent; autoimmune disease; organ transplant reference.
                                                                                                                                                                                                                                                                                      249
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97US-0062037
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                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.8%; 500
100.0%; Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                      GVHD;
                                                                                                                                                                                                                                 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 6.6e-113;
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                                                                                                                     lymphoid cell malignancy; shock; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 4
AAY95338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a TWEAK protein. The specification describes a method for preventing or treating an immunological disorder and/or inhibiting an immune response in an animal. The method comprises administering a TWEAK blocking agent. The method may be used for preventing and treating immune disorders associated with inappropriate expression and/or activity of TWEAK. These disorders include autoimmune diseases, acute and chronic inflammation, organ transplant rejection, Graft-versus-Host disease (GVHD), lymphoid cell malignancies, septic and other forms of shock, loss of immune responsiveness (as seen in human immunodeficiency virus (HIV) infections) and failure of the immune response to tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                                                                      Homo sapiens
                                                                                                                                    uterine
                                                                                                                                                PRO207; human;
breast cancer;
                                                                                                                                                                                            Human PRO207
                                                                                                                                                                                                                                                                               AAY95338 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rennert
                  Protein
                                             Peptide
                                                                                                                     central nervous
                                                                                                                                                                                                                        25-SEP-2000
                                                                                                                                                                                                                                                     AAY95338;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAARRSQRRRGERGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEEL 95
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249; Conserv
                                                                                                                                    cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                         antitumour protein.
                                                                                                                                                                                                                        (first entry)
                                                                                                                   antitumour; tumour; therapy; cytostatic;
ovarian cancer; renal cancer; colorectal cancer;
; prostate cancer; lung cancer; bladder cancer;
s system cancer; melanoma; leukaemia; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                   284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA,
               /label= Signal_peptide
                                                           Location/Qualifiers
   /label= PRO207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.8%; >u
100.0%; Pr
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                                                                                                                                                                                                                                                                                  249
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Pred. No. 6.6e-113;
0; Mismatches 0;
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                               Query Match
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28-APR-1999,
14-MAY-1999,
20-JUL-1999,
26-JUL-1999,
15-SEP-1999,
15-SEP-1999,
                                                                      The present sequence is that of human antitumour protein PRO207, as deduced from a foetal kidney cDNA clone (see AAA49717). PRC207 shows amino acid sequence identity to tumour necrosis factor family members, especially human lymphotoxin-beta (23.4%) and human CD40 ligand (19.8%). Mol.wt. is 27,216. A claimed method for inhibiting the growth of a tumour cell comprises exposing the tumor cell to PRO179, PRO207, PRO320, PRO219, PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO365, PRO509 or PRO866 (see AAY95337-49), their agonists or chimeric polypeptides incorporating them. The tumour is especially a cancer selected from breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder and central nervous system cancer, melanoma and leukaemia. Methods for the recombinant
                                                                                                                                                                                                                                                                                                         Novel composition to inhibit neoplastic cell growth or for treating tumor in mammal comprises polypeptides PRO179, PRO207, PRO320, PRO219, PRO221, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or
                                                         expression
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-442668/38.
N-PSDB; AAA49717.
                                                                                                                                                                                                                                                                                                                                                                                                             Napier MA,
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08-MAR-1999;
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                              Sequence
                                                                                                                                                                                                                                                               Claim 19; Fig 4; 172pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                            Ashkenazi AJ,
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                                                         of the antitumour proteins are also provided.
                               249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                               Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0113296.

99WO-US05028.

99US-013023.

99US-0131445.

99US-0134287.

99US-0144758.

99US-0145698.

99WO-US21090.

99WO-US21547.
                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard
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139..143
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45..51
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24..35
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10..14
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125..1
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36..42
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29..35
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   87
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 .88;
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 Score
 1268;
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 DВ
 21;
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 Length
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                                                                              08-MAR-1999
11-MAR-1999
11-MAY-1999
12-JUN-1999
22-JUN-1999
22-JUN-1999
26-JUL-1999
26-JUL-1999
27-JUL-1999
28-JUL-1999
17-AUG-1999
17-SEP-1999
15-SEP-1999
01-DEC-1999
01-DEC-1999
01-DEC-1999
01-DEC-1999
01-DEC-1999
01-DEC-1999
                         Marsters SA,
Watanabe CK,
                                                                                                                                                                                                                                                                                                                       Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocoelic disorder; inflammatory disorder; immune disorder; anglogenic disorder; cytostatic; neuroprotective.
                                                                                                                                                                                                                                                 11-FEB-2000;
                                                                                                                                                                                                                                                                   26-JUL-2001
                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                    Human
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2002-205567/26.
DB; ABK40255.
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                                                                                                                                                                                                                                                                                                                                                                    PRO207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity 100.0%; 249; Conservative 0;
                                                             GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                             99US-140650P

99US-140653P

99US-144758P

99US-145698P

99US-145698P

99US-14509P

99US-151689P

99WO-US2011

99WO-US2011

99WO-US2010

99WO-US2010

99WO-US2010

99WO-US20301

99WO-US20301
                                                                                                                                                                                                                                                                                                                                                                  polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                         Pan J,
Wood WI;
                                                                                                                                                                                                                                                 2000WO-US03565
                                           Goddard
                                                                                                                                                                                                             99US-123972P
99US-133459P
                                                                                                                                                                                                     99WO-US12252
                                                                                                                                                                                                                               99WO-US05028
                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                   Pitti
                                           P
                                 Godowski PJ,
L RM, Roy MA,
                                                                                                                                                                                                                                                                                                                                                                                                                        249
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Mismatches
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hes 0;
                                  Gurney
Smith
                                  ٧, AL,
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                                 Hillan K
Stone DM;
                                          ΚJ;
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RESULT 6
AAW29745
ID AAW2
XX AAW2
AC AAW2
AC AAW2
AC TNF
CONT 27-O
XX TNF;
KW TNF;
KW tiss
XX Homc
XX WO98
XX HOmc
XX HOmc
XX I O-F
PR 11-F
PR
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Best Local
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                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, gilal, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO polypeptides of the invention.
                                                                                                                       10-FEB-1998;
12-FEB-1997;
                                                                                                                                                                                                                                                                                                WO9835061-A2
                                                                                                                                                                                                                                                                                                                                                                                                 tissue
                                                                                                                                                                                                                                                                                                                                                                                                                          TNF; endothelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW29745
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                                                                         (ABBO ) ABBOTT
                                                                                                                                                                                                                                               13-AUG-1998
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                                                                                                                                                                                               12-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                              grafting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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97US-0798692
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                                                                                                                                                                                               98WO-US02859
                                                                                                                                                                                                                                                                                                                                                                                            proliferative agent; TREPA;
vascularisation; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
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100.0%;
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Pred. No. 6.6e-113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                                                                              wound healing; cancer;
autoimmune; birth control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Wiley SR;

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RESULT 7
AADEOMS 2
XX AABEM 2
XX AABEM 2
XX AABEM 2
XX AABEM 2
XX Humm 2
XX Humm 4
XX TREBM 4
XX TREBM 5
XX Homm 5
XX US66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC The TNF-related endothelium proliferative agent (TREPA), or its CC activators or agonists, are used to treat a deficit of TREPA, e.g. to CC promote wound healing or tissue grafting, by promoting vascularisation, CC also to induce apoptosis for treating cancer and eliminating autoreactive T cells, as an adjunct to cancer chemotherapy or antiviral treatment. CC TREPA peptides can also be used to target cytotoxic agents or for CC affinity isolation of the corresponding receptor, the nucleic acid for CC which can be used to transform tumour cells to render them more CC responsive to TREPA and to screen for TREPA mimics. CC RIDZYmes, antisense RNA, antibodies or peptides, are used to treat CC TREPA-associated diseases, e.g. tumours and metastases (by inhibiting CC conditions inclammation or a wide range of autoimmune conditions, CC conditions involving abnormal stimulation of epithelial cells (e.g. CC atheroscierosis), for birth control (inhibiting ovulation and placental corrections).
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N-PSDB;
                                                                                                                                           Human;
TREPA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting nucleic acid encoding TREPA - useful treatment of autoimmune disease, tumours and in
                                                                                                                            grafting;
                                                                                                                                                                                                                04-JUL-2001
                                                                                                                                                                                                                                                                      AAE00891 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 123-4; 142pp; English.
              US6207642-B1
                                                        Domain
                                                                                                HOMO
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DB; AAV47613.
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                                                                                                sapiens
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                                                                                                                                                                                   TREPA
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248; Conserv
                                                                                                                                           TNF
                                                                                                                                                       tumour necrosis factor;
                                                                                                                                           related
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                                                                                                                                                                                                             (first entry)
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A
                                      Location/Qualifiers 98..249
/label= Extracellul
                                                                                                                                                                                    related
                                                                                                                                         endothelium
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99.6%;
                                         Extracellular_domain
                                                                                                                                                                                    endothelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1265; D
Pred. No. 1.3e
1; Mismatches
                                                                                                                                                                                                                                                                      249
                                                                                                                                                       TNF;
                                                                                                                                        proliferative
                                                                                                                                                                                                                                                                       ₹
                                                                                                                                                       angiogenesis; wound healing;
                                                                                                                                                                                proliferative agent).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
1.3e-112;
hes 0;
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                                                                                                                                        agent;
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                                                                                                                                         tumour;
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                                                                                                                                         metastasis;
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RESULT 8
AAU03499
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molecules designated as TREPA (TNF related endothelium proliferative agent). Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis in human for promoting wound healing and for vascularising grafted tissue for successful grafting and to promote tissue grafts. The present amino acid sequence is clone ID #690050 human TREPA.
        retinoblastoma; retinopathy of prematurity; retrolental fibroplasia; rubeosis; uveitis; macular degeneration; arthritis; rheumatism; corneal graft neovascularisation; psoriasis; metastatic condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inducing angiogenesis in mammal at desired sites for promoting wound healing, by administering soluble fragment of extracellular domain of tumor necrosis factor related endothelium proliferative agent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wiley
                                              ocular neovascularisation; diabetic retinopathy; neovascular
                                                                                                                                                                    AAU03499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                             TWEAK extracellular domain; tumour necrosis factor; TNF; angiogenesis;
                                                                                        TWEAK
                                                                                                                  26-SEP-2001
                                                                                                                                          AAU03499;
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10-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                       VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 155
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)B; AAD04350.
                                                                                                                                                                                                                                                           TYFGLFQVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248;
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                                                                                     extracellular domain-containing fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0798692
98US-0021706
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75-76;
                                                                                                                                                                     Protein;
                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87.6%;
99.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1265; DB 22;
Pred. No. 1.3e-112;
1; Mismatches 0;
                                                                                                                                                                     273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                 215
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haemophilic joint;

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В
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                                                                                                                                                                                                                                                                                                                                                CC expression vector pDC409-LZ-TWEAK. The fusion protein comprises a CC expression vector pDC409-LZ-TWEAK. The fusion protein comprises a CC growth hormone leader, a leucine apper multimerisation domain, and CC growth hormone leader, a leucine apper multimerisation domain, and CC used in the isolation of human TWEAK. The fusion protein was CC used in the isolation of human cDNA library. The TWEAK protein is CC eliments from a COS cell human cDNA library. The TWEAK protein is CC angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of CC develop TWEAKR agonists and antagonists for the modulation of CC angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders CC characterised by ocular neovascularisation such as diabetic retinopathy, CC retrolental fibroplasia, rubeosis, uveitis, macular degeneration and CC corneal graft neovascularisation, and inflammatory diseases such as arthritts, rheumatism and psoriasis. Other treatable diseases include consist the human and prencephastic conditions, myocardial angiogenesis, CC haemophilic joints, scleroderma, vascular adhesions, atherosclerotic configure neovascularisation, telangiectasia, wound granulation, coronary atherosclerosis, peripheral atherosclerosis and ischaemia.
                                                                                                                                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating anglogenesis in a mammal for treating diseases mediated by anglogenesis, e.g. solid tumours and vascular deficiencies of cardiac peripheral tissue, by administering antagonist or agonist of TWEAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wiley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preneoplastic condition; myocardial angiogenesis; wound grascleroderma; vascular adhesion; telangiectasia; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 41; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-1999;
10-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-2000; 2000WO-US34755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peripheral atherosclerosis;
                                      187
                                                                                                                127
                                                                                                                                                      138
258
                                                                            198
                                                                                                                                                                                          67
                                                                                                                                                                                                                                78
                                                      LYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGS
                                                                                                                              ARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYURQIGEFIVTRAGLYY 197
                                                                                                                                                                                                            SLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTR 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-417975/44.
DB; AASO3964.
SLRIRTLPWAHLKAAPFLTYFGLFQVH
                                                                                                              ARRATAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYY
                                    LYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGS
                                                                                                                                                                                        SLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTR 126
                                                                                                                                                                                                                                                                        207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein.
                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                273 AA;
                                                                                                                                                                                                                                                                  73.8%; Score 1066; DB 22; llarity 100.0%; Pred. No. 1.5e-93; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0172878.
2000US-0203347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plaque neovascularisation; coronary atherosclerosis;
rosclerosis; pDC409-LZ-TWEAK; TWEAK receptor; TWEAKR;
                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          granulation;
                                                                                                                                                                                                                                                                                                        273;
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77 VSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKT 136

Matches Query Match

Local

l Similarity 207; Conserv

Conservative

73 99 .58

Score 1062; DB Pred. No. 2.6e-9 0; Mismatches

1.6e-93; 1;

Indels Length

Gaps

0

208; 0,

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RESULT 9
AAW93590
  В
                                                CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated Tum related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 is useful for diagnosing prostate cancer CC by their active fragments. APO4 is useful for diagnosing prostate cancer CC be treated using APO4 selective binding agents linked to a therapeutic CC molety. APO4 polypeptides are also useful for identifying selective CC binding agents, useful in diagnosis/treatment of disease by binding of agents to the polypeptide/active fragment which is extracellular, or CC expressed on the cell surface. The binding is preferably performed in CC vivo. APO4 polypeptides/active fragments are also useful for screening CC for agonists and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or CC treatment of disease are also identified using APO4 polypeptides/active CC treatment of disease are also identified using APO4 polypeptides/active control of the cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vitro. APO polypeptides are all useful as immunogens for preparing antibodies. APO4 is also cuseful for diagnosis/treatment of developmental or gestational coll line controls.
                                  abnormalities.
MCF-7, and indu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 40; Fig 13A; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Tumor Necrosis Factor family receptor polypeptides and ligands useful for diagnosis and treatment of prostate cancer and developmental or gestational abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-205191/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4 developmental abnormality; gestational abnormalitity; prostate cancer; APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disea: cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW93590
  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apoptosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human TNRL3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIW ) UNIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WASHINGTON
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                                      apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy; disease;
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suppress the immune system. It is useful to screen for TRELL receptors, by labelling with a detectable label and screening compositions for binding. Agents interfering with TRELL-receptor binding can also be screened for, can then be administered, optionally with interferon- gamma, to induce cell death or treat, suppress or alter immune responses (especially involving human adenocarcinoma cells) involving a signal pathway between TRELL and its receptor. It's coding sequence can be used in gene therapy for TRELL-related disorders in mammals (especially humans), e.g. tumours, autoimmune and inflammatory diseases or inherited genetic disorders, by introducing into cells, and expressing, therapeutically effective
                                                                                                                                                                                                                                                                                                                                                                           18-MAR-1997;
07-AUG-1996;
18-OCT-1996;
                                                                                                                                         The sequence is that of mouse tumour necrosis factor related ligand (TRELL). TRELL or active fragments can be included with a carrier in pharmaceutical compositions to treat cancer, autoimmun diseases or immune responses to tissue grafts, or to stimulate or
                                                                                                                                                                                                                                   Tumour necrosis factor related ligand cancer, auto-immune disease and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                          Claim 12; Pages 48-50; 69pp; English.
                                                                                                                                                                                                                                                                                                              Browning JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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DB; AAV18599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rejection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
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96US-0023541.
96US-0028515.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "hydrophobic, transmembrane domain"
                                                                                                                                                                                                                                   and immune responses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune system; stimulation; suppression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 factor related ligand
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    useful for,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TRELL).
                                                                                                                                                                                                                                   tissue
                                                                                                                                                                                                                                                  e.g.
                                                                                                                                                        autoimmune
                                                                                                                                                                                                                                   treating
ue grafts
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RESULT 11
AAB07527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amounts of a vector, e.g. a virus comprising a gene It may also be of use in the preparation of prepare screening natural/synthetic DNAs for TRELL-encoding
            be used for preventing and treating immune discorders associated inappropriate expression and/or activity of TWEAK. These discorde include autoimmune diseases, acute and chronic inflammation, org transplant rejection, Graft-versus-Host disease (GVHD), lymphoic
                                                           describes a method for preventing or treating an immunological disorder and/or inhibiting an immune response in an animal. The method comprises administering a TWEAK blocking agent. The method may
                                                                                                                                                     Preventing and treating immune responses using modulators, antibodies, of TWEAK, TWEAK receptors and TWEAK ligands, ustreating e.g. inflammation and graft versus host disease -
                                                                                                                                                                                                                                                                                                                                                                                                                     TWEAK blocking agent; autoimmune disease; organ transplant rejection; Graft-versus-Host disease; GVHD; lymphoid cell malignancy; shock; tumour.
                                                                                                                                                                                                                                                                                                                                                                                             Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a soluble recombinant murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB07527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                    The present sequence represents a TWEAK protein.
                                                                                                                               Disclosure;
                                                                                                                                                                                                           WPI; 2000-476036/41
                                                                                                                                                                                                                                      Rennert
                                                                                                                                                                                                                                                            (BIOJ ) BIOGEN INC
                                                                                                                                                                                                                                                                                        15-JAN-1999;
                                                                                                                                                                                                                                                                                                                 14-JAN-2000;
                                                                                                                                                                                                                                                                                                                                           20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                    WO200042073-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                    TWEAK protein;
TWEAK blocking
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for antisense therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQVH
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                                                                                                                                                                                                                                     P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 AA;
                                                                                                                              Fig 1; 45pp; English.
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                                                                                                                                                                                                                                                                                                                  2000WO-US01044
                                                                                                                                                                                                                                                                                          99US-0116168
                                                                                                                                                                                                                                                                                                                                                                                                                                              immunological disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.6%;
other forms of shock, l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225
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Pred. No. 2.9e-89
9; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                              immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
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                                                                                                       The specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225
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probes for
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              lymphoid
                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation;
                                                                                                                                                            useful
                                    disorders
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                                                   with
              cell
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Best Local S
Matches 199
This invention describes isolated Tumor Necrosis Factor (TNF) family receptor polypeptides: APO4, APO6, APO8 and APO9 or their active fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic molety. APO4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding of
                                                                                                                                                                                                                                             Chaudhary
                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4; developmental abnormality; gestational abnormalitity; prostate cancer; APO6; APO6; APO6; APO6; APO8; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease; cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW93591 standard;
                                                                                                                          Claim
                                                                                                                                                    developmental
                                                                                                                                                                useful
                                                                                                                                                                                                                                                                                                 05-SEP-1997;
                                                                                                                                                                                                                                                                                                                          04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                               W09911791-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis;
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                                                                                                                                                                                                                                                                       (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                     11-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse TNRL3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections) and failure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 LGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ν
                                                                                                                                                Tumor Necrosis Factor family receptor polypeptides and ligands ful for diagnosis and treatment of prostate cancer and elopmental or gestational abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLR
                                                                                                                                                                                                                  1999-205191/17.
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                                                                                                                       40; Fig
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                                                                                                                          13B;
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                                                                                                                     156pp;
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Of
                                                                                                                       English.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody preparation; breast carcinoma;
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Best Local S
Matches 188
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                                         Claim 16;
                                                                                                                                                                                      Wiley
                                                                                                                                               WPI; 1998-447255/38
                                                                                                                                                                                                                                                                         10-FEB-1998;
12-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW29746;
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                                                                                                                                                                                                                                                                                                                                   12-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKARPRRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEETKINSSSPLRYDRQIGEFTVIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    grafting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                nucleic acid encoding TREPA - useful of autoimmune disease, tumours and in
                                       Page 125-6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211
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                                                                                                                                                                                                                                                                      98US-0021706
97US-0798692
                                                                                                                                                                                                                                                                                                                                     98WO-US02859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferative agent; TREPA; wound healing; car vascularisation; apoptosis; autoimmune; birth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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89.1%;
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Pred.
                                       English.
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No. 2.
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                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 211;
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                                                                                                      diagnosis
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TNF-related

endothelium

proliferative

agent (TREPA),

or its

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RESULT 14
AAE00892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     activators or agonists, are used to treat a deficit of TREPA, e.g. to promote wound healing or tissue grafting, by promoting vascularisation, also to induce apoptosis for treating cancer and eliminating autoreacti T cells, as an adjunct to cancer chemotherapy or antiviral treatment. TREPA peptides can also be used to target cytotoxic agents or for affinity isolation of the corresponding receptor, the nucleic acid for which can be used to transform tumour cells to render them more responsive to TREPA and to screen for TREPA mimics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ribozymes, antisense RNA, antibodies or peptides, are used to treat TREPA-associated diseases, e.g. tumours and metastases (by inhibiting vascularisation), inflammation or a wide range of autoimmune conditions, conditions involving abnormal stimulation of epithelial cells (e.g. atherosclerosis), for birth control (inhibiting ovulation and placental formation) or other angiogenic conditions (e.g. ulcers).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human UL4flag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE00892 standard;
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                                                                                                                                                                                                                                                                        12-FEB-1997;
10-FEB-1998;
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Inducing angiogenesis in mammal at desired sites for promoting wound healing, by administering soluble fragment of extracellular domain o tumor necrosis factor related endothelium proliferative agent protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumour necrosis factor; TNF; angiogenesis; wound healing; tumour;
TNF related endothelium proliferative agent; metastasis; grafting;
ary; HUVEC; human umbilical vein endothelial cell; UL4flag.
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Pred. No. 1.4e-67;
D; Mismatches 1;
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to extracellular signal molecules,

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         The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNF) family molecules designated as TREPA (TNF related endothelium proliferative agent). Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis
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10-FEB-1998;
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Search completed: March 31, 2003, 07:44:12 Job time: 55.5639 secs
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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-Q-cgn2_1/USPT0_Spool/US9245198/runat_24032003_163553_25950/app_query.fasta_1.846
-DB=GenEmb1 -QFMT-fastap -SUFFIX-rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXY=0
-UNITS-blits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTPMT-pto -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER-US09245198_eCGN_1_1_3077_erunat_24032003_163553_25950 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THERANS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPD=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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seq length: 2000000000
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Ygapop 10.0 , X
Fgapop 6.0 , F
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Sequence 3 f
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South San Francisco, CA 9408
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                                                                                                                       /product="Apo3/DR3 11gand"
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YYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAAASSLGPQLRLCQVSGLLAL
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443 c 389 g 264 t
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                                                                                                                                                                                                                                                                        /gene="APO3L"
58. .807
                                                                                                                                                                                                                                    /function="binds to Apo3/DR3"
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Sheridan,J.P.,
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Mammalia; Eutheria;
                Homo sapiens.
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                                                                  1651 bp mRNA, Similar to tumor necrosis member 12, clone MGC:20669
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Primates;
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IMAGE:4766071,
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         Euteleostomi;
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GlyGluProGlyThrAlaLeuLeuValProLeuAlaLeuGlyLeuGlyLeuAlaLeuAla
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This clone was selected for full length sequencing bec passed the following selection criteria: matched mRNA Location/Qualifiers
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Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Broc
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legas
Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt
CDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortiu
DNA Sequencing by: National Institutes of Health
Sequencing Center (NISC),
Gaithersburg, Maryland;
uph Site.
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Contact: MGC help desk
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superfamily, member 12"
/protein_id="AAH19047.1"
/db_xref="GI:17512139"
/translation="MAARRSORRRGREPGTALLVPLALGLGLALACLGLLLAVVSL
GSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTR
ARRALAHYEVHPRPPQDGAQADGGYTTCLRP"
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/tissue_type="Primary B-Cells fr/
/clone_lib="NIH_MGC_48"
/lab_host="DH10B-R"_
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/db_xref="taxon:9606"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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TWEAK, a new secreted ligand in the tumor necrosis that weakly induces apoptosis
J. Biol. Chem. 272 (51), 32401-32410 (1997)
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GSRASLSAQEPAQEELvAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTR
ARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGL
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/protein_id="AAC51923.1"
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18. .767
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                            Direct Submission
Submitted (14-OCT-1997) Cell
Cambridge, MA 02142, USA
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1 (bases 1 to 1168)
Chicheportiche, Y., Bourdon, P.R., Xu, H.
Hession, C., Garcia, I. and Browning, J.
TWEAK, a new secreted ligand in the that weakly induces apoptosis
J. Biol. Chem. 272 (51), 32401-32410
                                                               2 (bases 1 to 1168)
Chicheportiche, Y., Bixler, S.,
Direct Submission
                                                                                                                          J. Biol. Chem.
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                                                      IleArgThrLeuProTrpAlaHisLeuLysAlaAlaProPheLeuThrTyrPheGlyLeu
                                                                                                                                                                                                                                                                                                 TyrAsnArgGlnIleGlyGluPheIleValThrArgAlaGlyLeuTyrTyrLeuTyrCys
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/db_xref="taxon:10090"
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                                                                                                                                        Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 2, 2002 this sequence version replaced gi:15421989. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 117703)
Birren,B., Nusbaum,C. and Lander,E.
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AC016876
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NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 177703)
                                           Center clone name: 186_B_7
                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                        Center project
                                                                                                 Web site: http://www-seq.wi.mit.edu
                                                                                                                Center code: WIBR
                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
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*** SEQUENCING IN PROGRESS ***, 10
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US-09-245-198A-4 (1-284) x AC016876 (1-177703)
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rAlaAlaSerSerLeuGlyProGlnLeuArgLeuCysGlnValSerGlyLeuLeuAlaLe 253
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                                                                                                GCTGGACTTGCTGGTGGATGGTGTGCTGGCCTGCCTGCGCTGCCTGGAGGAATTCTCAGCCAC 37217
                                                                                                                                           sLeuAspLeuLeuValAspGlyValLeuAlaLeuArgCysLeuGluGluPheSerAlaTh 233
                                                                                                                                                                                                                                                                                   ACTCGGCCTGTTGTCCCCACCCCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAA 37277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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111050 111149: gap of 100 bp
111150 125020: contig of 13871 bp in length
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4846 48745: gap of 100 bp

48746 58277: contig of 9532 bp in length

58278 58377: gap of 100 bp

58378 65804: contig of 7427 bp in length
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/db_xref="taxon:9606"
/clone="RP11-186B7"
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45967 c 46568 g 41254 t 1052
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Pan.

E 1 (bases 1 to 215795)

E Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,
Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,
Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P.,
Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,
Lee-Lin, S.-H., Masiello, C., Maskeri, B., Mastrian, S.D.,
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Portnoy, M.E., Prasad, A., Schueler, M.G., Stantripop, S., Thomas, J.W.,
Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.
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                                                                                                        * NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (17-JUL-2002) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC127470 215795 bp Pan troglodytes clone RP43-145D13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NISC Comparative Sequencing Initiative
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                                                                         as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                             Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 203929 bases at least Q40 Consensus quality: 203665 bases at least Q30 Consensus quality: 203181 bases at least Q20 Insert size: 190000; agarose-fp Insert size: 214395; sum-of-contigs Quality coverage: 7.30x in Q20 bases; sum-of-contig Quality coverage: 6.47x in Q20 bases; sum-of-contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 215795)
                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: cms
Center clone name: 145D13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: nisc_zoo@nhgri.nih
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.nisc.nih.gov
       3594
3694
8002
                                                                                                                                                                                                                                                                                                                                                                                                          ----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- Project Information
3593: contig of 3593 bp in length 3693: gap of unknown length 8001: contig of 4308 bp in length 8101: gap of unknown length
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                                                      Percent Similarity:
Best Local Similarity:
Query Match:
     US-09-245-198A-4 (1-284)
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89623. .105537
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49443. .60956
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39313. .49342
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3694. .8001
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166903. .215795
/note="assembly_fragment"
54859 c 53752 g 53513 t
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138984. .166802
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15740. .24775
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/db_xref="taxon:9598"
/clone="RP43-145D13"
/clone_lib="RP43"
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of 27819 bp in
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of 17586 bp in
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Akhter, M., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Akhter, M., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Berjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wigyins, L., Young, A., Zhang, L.-H. and Green, E.D. Insublished
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Sus scrofa clone RP44-436K21,
                                 Submitted (08-AUG-2002) NIH Intramural Sequencing Center, Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                     Green, E.D.
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Mammalia;
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Center: NIH Intramural Sequencing Center
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Eutheria; Cetartiodactyla; Suina; Suidae;
                      Genome Center
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21302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Insert size: 169000; agarose-fp
Insert size: 176655; sum-of-contigs
Quality coverage: 4.78x in Q20 bases; agarose-fp
Quality coverage: 4.57x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
------ Project Information
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3561. .6869
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/db_xref="taxon:9823"
/clone="RP44-436K21"
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76771. .115165
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115266. .177555
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45154: gap of unknown length
58724: contig of 13570 bp in 16
58824: gap of unknown length
76670: contig of 17846 bp in 16
76770: gap of unknown length
115165: contig of 38395 bp in 16
1177555: contig of 62290 bp in 16
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                                                                                 nLeuArgLeuCysGlnValSerGlyLeuLeuAlaLeuArgProGlySerSerLeuArgII
                                                                                                                              lLeuAlaLeuArgCysLeuGluGluPheSerAlaThrAlaAlaSerSerLeuGlyProGl
                                                                                                                                                                             nValH1sPheAspGluGlyLysAlaValTyrLeuLysLeuAspLeuLeuValAspGlyVa
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 eGlnValHis
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Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R. W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulles, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D. NISC Comparative Sequencing Initiative
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* This record will be updated with the finished sequence

* as soon as it is available and the accession number wil.

* be preserved.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 148712 bases at least Q40
Consensus quality: 151471 bases at least Q30
Consensus quality: 151471 bases at least Q20
Consensus quality: 153125 bases at least Q20
Insert size: 152000; agarose-fp
Insert size: 160028; sum-of-contigs
Ouality coverage: 5.10x in Q20 bases; sum-of-contig
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Center clone name: 332E1
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EQUENCE, 15
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0882 49783: contig of 8902 bp in length
0784 49883: gap of unknown length
0784 49883: gap of unknown length
0784 59150: contig of 9267 bp in length
0785 68679: contig of 9429 bp in length
0786 68779: gap of unknown length
0786 7984: contig of 10205 bp in length
0785 79084: gap of unknown length
0785 79084: gap of unknown length
0785 79084: gap of unknown length
0786 102175: contig of 8629 bp in length
0787 102175: contig of 8629 bp in length
0788 131685: contig of 29410 bp in length
0788 131685: contig of 29643 bp in length
0788 161428: contig of 29643 bp in length
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93547. .102175
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/organism="Canis familiaris"
/organism="Canis familiaris"
/db_xref="taxon:9615"
/clone="RP81-332E11"
/clone_lib="RP81"
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131786. .161428
/note="assembly_fragment"
41863 c 41233 g 37340 t
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Matches:
Conservative:
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OMMENT	JOURNAL REFERENCE AUTHORS TITLE JOURNAL	TITLE			HOLHONG	ERENC	KEYWORDS SOURCE ORGANISM	ACCESSION	SULT 12 :069459/c :CUS :FINITION	42266	274	42326	254	42386	, ,	214	42506	201	42566	200	42626	200	42686	192	42746
USA rsion licin) Human Ger	Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S., Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A., Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G., Worley,K. and Gibbs,R. Direct Submission	Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R., Massey, E., McLeod, M. P., Mei, G., Moore, S., Morgan, M., Morris, S., Neal, D., Nelson, A., Nguyen, R., Nguyen, N., Oguh, M., Parish, B.,	<pre>Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S., Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R., Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M.,</pre>	Dederich, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, Z.,	Manmalia: Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Hammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 203083)	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP. HTG HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP. Mus musculus. Mus musculus. Fulbaryota. Motagoa. Chordata. Craniata. Voctobrata. Eutologa	5 6 8	AC069459 203083 bp DNA linear HTG 27-JUN-2001 Mus musculus chromosome 11 clone RP23-168P5, WORKING DRAFT	CCTTACCTACTTCGGACTCTTCCAGGTTAAC 42236	eLeuThrTyrPheGlyLeuPheGlnValHis 284	GCCGGGTCCTCCTGCGGATCCGCACCCTCCCCTGGGCCCATCTCAAGGCCGCCCCCTT 42267	gProGlySerSerLeuArgIleArgThrLeuProTrpAlaHisLeuLysAlaAlaProPh 274	dAlaberSerieus PyrosinieuArgheucyssinyalsers lyheuleuAraleuAr 234) i	uAspLeuLeuValAspGlyValLeuAlaLeuArgCysLeuGluGluPheSerAlaThrAl 234 	GCGGCCTCCTGCCGGCCCCAGGTGCACTTTGATGAGGGGAAGGCTGTCTACCTGAAGCT 42447	GlnValHisPheAspGluGlyLysAlaValTyrLeuLysLe 214	GTGGGGAGCCTAGGGTCGGGGCCCGATGGGATCCTGGGGTCACCAAGGACCCCGGACTCT 42507	200	GGAAGCGGGGGCCCCAGGTTGAGGGAGACGGAGAGGGTTTGGTTCAGGGGGCCAGGTTGGG 42567	200	CGGGCTGGGCTCTACTACCTGTACTGCCAGGTAAGCCCCACCTGGCTCCACGGTAGGGCA 42627	ArgAlaGlyLeuTyrTyrLeuTyrCys 200	AAAATCAACAGCTCCAACCCACTGCGCTATGACCGCCAGAGCGGGGAATTTATAGTCACG 42687

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US-09-245-198A-4 (1-284) x AC069459 (1-203083)
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Best Local Similarity:
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TACTGTCAGGTAAGCCCTGCCTGGCTTCAGGGGGCAGAGCCAAAGGCTAAGGGGAGGAGGAG 43126
                                              TyrCys-----
                                                                                          CTGCGCTACGACCGCCAGATTGGGGAATTTACAGTCATCAGGGCTGGGCTCTACTACCTG 43186
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-primer Bodipy: 48% of reads chemistry: Dye-terminator Big Dye: 52% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 212648 bases at least Q40 Consensus quality: 218902 bases at least Q30 Consensus quality: 222384 bases at least Q30 Estimated insert size: 210656; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; sqarose-fp estimation Quality coverage: 7.2x in Q20 bases; sum-of-contigs estimation
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/db_xref="taxon:10090"
/chromosome="11"
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62352: gap of unknown length
118772: contig of 56520 bp in length
118872: gap of unknown length
148924: contig of 30052 bp in length
149924: gap of unknown length
169231: contig of 18207 bp in length
167331: gap of unknown length
167331: gap of unknown length
189907: contig of 22576 bp in length
199007: gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cambridgeshire, CBIO 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 20, 2001 this sequence version replaced gi:16605765.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were aither denthlesteration?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw:, courselves the sequence of the subcurrent of the su
                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-422L16 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (17-NOV-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL603707
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Mouse DNA sequence from clone
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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complement(84050.
                                  /clone="RP23-422L16"
/clone_lib="RPCI-23"
                                                                                                                          /chromosome="11"
                                                                                                                                                                                                             /organism="Mus musculus"
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e RP23-422L16 on chromosome
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Query Match:
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           Akhter.N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
Berooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J.,
Haghlighi,P., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Laric,P.,
Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
Margulies,E.H., Masiello,C., Maskeri,B., Mastrian,S.D.,
McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R.,
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AC126921.1 GI:21724098
                                                                                                                                                                                                                                                                                                                                          AC126921 153553 bp DNA Bos taurus clone RP42-45D24, WORKING DI
                                                                                                                                                 Bovidae; Bovinae; Bos. 1 (bases 1 to 153553)
                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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 Portnoy,M.E., Prasad,A., Schueler,M.G.,
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big dye terminator reads only."
s 56824 c 57519 g 60529 t
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DRAFT SEQUENCE,
Stantripop, S., Thomas, J.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-JUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and the accession number will be preserved.
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Consensus quality: 146066 bases at least Q40
Consensus quality: 147748 bases at least Q30
Consensus quality: 148824 bases at least Q20
Insert size: 151000; agarose-fp
Insert size: 152453; sum-of-contigs
Quality coverage: 8.00x in Q20 bases; agarose-fp
Quality coverage: 8.72x in Q20 bases; sum-of-contigs
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90860
90960
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Center clone name: 045D24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: NIH Intramural Sequencing Center code: NISC Center code: NISC Web site: http://www.nisc.nih.gov Contact: nisc_zoo@nhgri.nih.gov
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                                     clone_end:T7
                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
/clone="RP42-45D24"
/clone_lib="RP42"
                                                                                                                                                                                                          Location/Qualifiers
1. .153553
                                                     /note="assembly_fragment
                                                                                        /note="assembly_fragment"
                                                                                                                                                                                                                                                          56690: gap of unknown length
73769: contig of 17079 bp in 14
73869: gap of unknown length
90859: contig of 16990 bp in 14
90959: gap of unknown length
111428: contig of 20469 bp in 14
111528: gap of unknown length
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                                                                                                               LeuGluGluPheSerAlaThrAlaAlaSerSerLeuGlyProGlnLeuArgLeuCysGln 246
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RS MIZNY, D.M., Addams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Binage, K., Blanksaburg, K., Bonnin, D., Barbaria, J., Boute, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bohay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Davila, M., Carroll, J., Garza, N., Gill, R., Carroll, J., Garza, M., Garner, T., Garza, N., Gill, R., Carroll, J., Garzia, M., Garner, T., Garza, N., Gill, R., Goist, J., Garcia, A., Garner, T., Garza, N., Hernandez, J., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Harris, K., Hart, M., Halloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Vila, Y., Johnson, R., Jolivet, S., Joudah, S., Kals, C., Hart, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Willia, L., Kovar, C., Kratovic, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Locier, R., Luna, R., Ma, J., Lavis, J., Liu, Y., Jukes, J., Lucier, R., Luna, R., Ma, J., Lavis, J., Lavis, J., Lucier, R., Luna, R., Ma, J., Levis, L.C., Lewis, L., Luna, R., Ma, J., Lavis, J., Massey, E., Mawhiney, E., McLeod, M. P., Maedor, M., Mei, G., Metzker, M., Massey, E., Mayer, N., Wokenkwo, S., Oguh, M., Okwuonu, G., Martinoz, E., Martinoz, E., Willey, M., Stone, H., Shoshita, R., Primar, E., M., Thomas,
                                                                             Submitted (18-JUL-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA on Jul 14, 2002 this sequence version replaced
                                                                                                                                                                                                                                       Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                        Submitted (25-APR-2002) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 138792)
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Worley, K.C.
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Center: Baylor College of Medicine
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NOTE: Estimated insert size may differ from sequence length (see http://www.lbgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'vorking draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of recharge program: Phrap; version 0.990329
Consensus quality: 112720 bases at least Q40
Consensus quality: 116666 bases at least Q30
Consensus quality: 119165 bases at least Q20
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Center clone name: CH230-320N23
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Search completed: March Job time: 4151.52 secs

31,

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OM protein - nucleic search, using frame_plus_p2n model GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

March 31, 2003, 00:47:43; Search time 294.043 Seconds

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2175.080 Million cell updates/sec

Title: Perfect score: US-09-245-198A-4 1444 Run

on:

MSLLDFEISARRLPLPRSLG......PWAHLKAAPFLTYFGLFQVH 284

Scoring table: Xgapop 10.0 , X Ygapop 10.0 , Y Fgapop 6.0 , F Delop 6.0 , D BLOSUM62 Xgapext Ygapext Fgapext Delext

Searched: 2185239 seqs, 1125999159 residues 0.5 7.0 7.0

Total number of hits satisfying chosen parameters:

4370478

Minimum DB Maximum DB seg length: 0 seg length: 2000000000

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Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
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-DB-N_Geneseq_101002 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1 AAV18600

AAV18600 standard; cDNA; 1373 ВP

AAV18600;

21-JUL-1998 (first entry)

Homo sapiens tumour necrosis factor related ligand (TRELL) gene

TRELL; tumour necrosis factor related ligand; tnf; treatment; cancer; autoimmune disease; immune system; stimulation; suppression; graft rejection; ds.

Homo sapiens

Location/Qualifiers 1..852

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ssue sources which encode secreted proteins, useful for
immune deficiencies and disorders such as autoimmune
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The present sequence encodes a human tumour necrosis factor (TNF) an Lymphotoxin homologue designated Apo-3 ligand. Apo-3 ligand has cytostatic activity. Apo-3 ligand can be used to induce apoptosis in mammalian cancer cells, to induce NF-kappaB-dependent transcription
                                                                                                                Ashkenazi
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                                                                 Apo-3 ligand
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/product= "Apo-3 ligand"
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                                                                 (a tumour
                                               English
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RESULT 4
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                                                                                               ValSerGlyLeuLeuAlaLeuArgProGlySerSerLeuArgIleArgThrLeuProTrp
                                                                                                                                            LeuGluGluPheSerAlaThrAlaAlaSerSerLeuGlyProGlnLeuArgLeuCysGln
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                                                                                     GTGTCTGGGCTGTTGGCCCTGCGGCCAGGGTCCTCCCTGCGGATCCGCACCCTCCCCTGG
                                                                                                                                CTGGAGGAATTCTCAGCCACTGCGGCGAGTTCCCTCGGGCCCCAGCTCCGCCTCTGCCAG
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Matches:
Conservative:
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Indels:
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                                 Alignment
                                               The present sequence is that of cDNA clone DNA30879-1152 CC (AFCC 209358) encoding human PRO207 (see AAY95338), which shows CC (homology to several members of the tumour necrosis factor family, CC especially human lymphotoxin (23.4%). The cDNA was identified in a CC feetal kidney cDNA library following identification of an expressed CC sequence tag with homology to human Apo-2 ligand. A claimed method CC for inhibiting the growth of a tumour cell comprises exposing the CC tumor cell to PRO179, PRO207, PRO320, PRO219, PRO221, PRO224, PRO328, PRO301, PRO526, PRO362, PRO356, PRO509 or PRO866 (see CC AAY95337-49), their agonists or chimeric polypeptides incorporating CC them. The tumour is especially a cancer selected from breast, CC ovarian, renal, colorectal, uterine, prostate, lung, bladder and CC central nervous system cancer, melanoma and leukaemia. Nucleic acids encoding PRO179 etc. are used in the recombinant production CC of the antitumour polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-1999;
21-APR-1999;
28-APR-1999;
14-MAY-1999;
20-JUL-1999;
26-JUL-1999;
15-SEP-1999;
15-SEP-1999;
                              Sequence 1353
                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                             Novel composition to inhibit neoplastic cell growth or tumor in mammal comprises polypeptides PRO179, PRO207, PRO321, PRO324, PRO328, PRO301, PRO526, PRO362, PRO366,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
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                                                                                                                                                                                                                                                                                                          2000-442668/38.
DB; AAY95338.
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                                                                                                                                                                                                                                                                                                                                         J, Goddard A,
Pitti RM, Woo
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                               BP;
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99WO-USO5028.

99US-0130232.

99US-0131445.

99US-0134287.

99US-01146758.

99US-0145698.

99WO-US21547.
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58.807
/*tag= a
58.177
/*tag= b
178.804
/*tag= c
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                               C;
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Gurney

for treating PRO320, PRO2 or

Length:

1353

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Query Match:
RESULT 5
ABK40255
ID ABK4
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AC ABK4
XX
DT 15-JI
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DE CDNA
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Best Local Similarity:
 cDNA encoding
                           ABK40255;
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                                                                                                                                                                                                                                                                                                                                                             AlaGlnAlaGlyValAspGlyThrValSerGlyTrpGluGluAlaArgIleAsnSerSer
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              (first entry)
 human PRO207
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100.00%
100.00%
94.60%
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polypeptide
                                        ВP
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Gaps:
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                                             Best Local Similarity: Query Match:
                           US-09-245-198A-4
                                                                 Score:
                                                                              Alignment
                                                          Percent Similarity:
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(1-284) x ABK40255

(1-1353)

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Mismatches: Indels: Gaps:

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02-JUN-1999
22-JUN-1999
22-JUN-1999
22-JUL-1999
26-JUL-1999
26-JUL-1999
28-JUL-1999
17-AUG-1999
17-SEP-1999
15-SEP-1999
01-DEC-1999
01-DEC-1999
01-DEC-1999
05-JAN-2000
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11-MAR-1999;
11-MAY-1999;
                                                                                                                                                                The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. ABR40254-ABR40288 encode for the human PRO polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marsters
Watanabe
                                                                                                                                                                                                                                                                                                                                                                                  Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, angiogenic and immunologic disorders
                                                                                                                                    Sequence 1353
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Leukaemia; neuronal disorder; stromal disorder; bla 
inflammatory disorder; immune disorder; angiogenic 
gene therapy; cytostatic; neuroprotective; gene; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB;
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DB; AAU86129.
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99US-144758P
99US-145698P
99US-146222P
99US-149395P
99US-151689P
99WO-US20111
99WO-US20111
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99WO-US20313
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rafting; vascularisation; apoptosis; autoimmune; birth or
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                                                                                                                                                                                                                                                                                                                                                                                Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                         The TNF-related endothelium proliferative agent (TREPA), or its cactivators or agonists, are used to treat a deficit of TREPA, e.g. to promote wound healing or tissue grafting, by promoting vascularisation, calso to induce apoptosis for treating cancer and eliminating autoreactive Teells, as an adjunct to cancer chemotherapy or antiviral treatment. TREPA peptides can also be used to target cytotoxic agents or for caffinity isolation of the corresponding receptor, the nucleic acid for which can be used to transform tumour cells to render them more cresponsive to TREPA and to screen for TREPA mimics. Ribozymes, antisense RNA, antibodies or peptides, are used to treat TREPA-associated diseases, e.g. tumours and metastases (by inhibiting vascularisation), inflammation or a wide range of autoimmune conditions, conditions involving abnormal stimulation of epithelial cells (e.g. atherosclerosis), for birth control (inhibiting ovulation and placental contents).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting treatment
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P-PSDB; AAW29745.
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12-FEB-1997;
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TNF related endothelium
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/product= "Human TREPA (TNF related endothelium
proliferative agent)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to extracellular signal molecules, particularly members of tumour necrosis factor (TNP) family molecules designated as TREPA (TNP related endothelium proliferative agent). Soluble biologically active TREPA are used to treat TREPA-associated diseases, tumours or metastases. TREPA is used for inducing angiogenesis in human for promoting wound healing and for vascularising grafted tissue for successful grafting and to promote tissue grafts. The present sequence is a cDNA clone ID #690050 encoding human TREPA.
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                                                                                                                                                                                                                                                                                                          GlyAlaGlnAlaGlyValAspGlyThrValSerGlyTrpGluGluAlaArgIleAsnSer 175
                                                                                                                                                                                                                                                                                                                                              LeuValProLeuAlaLeuGlyLeuGlyLeuAlaLeuAlaCysLeuGlyLeuLeuLeuAla
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                                                                                                                                                   LeuLeuValAspGlyValLeuAlaLeuArgCysLeuGluGluPheSerAlaThrAlaAla
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the isolation of human TWEAK receptor (TWEAKR)-expressing clones from a COS cell human cDNA library. The TWEAKR protein is a member of the tumour necrosis factor (TNP) family and induces angiogenesis. TWEAKR may therefore be used to screen for and develop TWEAKR agonists and antagonists for the modulation of angiogenesis, to be used in the treatment and diagnosis of human disease. The disorders mediated by angiogenesis include ocular disorders characterised by ocular neovascularisation such as diabetic retinopathy, neovascular glaucoma, retinoblastoma, retinopathy of prematurity, retrolental fibroplasia, rubeosis, meaular degeneration and corneal graft neovascularisation, and inflammatory diseases such as arthritis, rheumatism and psoriasis. Other treatable diseases include malignant and the corneal diseases include malignant and content of the corneal diseases include malignant and the corneal diseases include malignant and diseases include malignan
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                                                                                                                                                                                                                                                                                                                                   pDC409-LZ-TWEAK, which encodes a fusion protein comprising a growth hormone leader, a leucine zipper multimerisation domain, and the extracellular domain of human TWEAK. The fusion protein was used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulating angiogenesis in a mammal for treating diseases mediated angiogenesis, e.g. solid tumours and vascular deficiencies of cardiperipheral tissue, by administering antagonist or agonist of TWEAK
rheumatism
metastatic
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10-MAY-2000;
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DB; AAU03499.
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2000US-0203347.
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                            Human TNRL3
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                                                                                           AAX23424 standard;
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Tumour necrosis developmental

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                                                                                                                                                                                                                                                    CC This invention describes isolated Tumor Necrosis Factor (TNF) family CC receptor polypeptides: APO4, APO6, APO8 and APO9 or their active CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or CC their active fragments. APO4 is useful for diagnosing prostate cancer CC by determining levels of APO4 in an individual. Prostate cancer can also by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic CC moiety. APO4 polypeptides are also useful for identifying selective CC depends to the polypeptides are also useful for identifying selective CC expressed on the cell surface. The binding is preferably performed in CC expressed on the cell surface. The binding and observing the changer in APO4 CC expressed on the cell surface. The binding and observing the changer in APO4 CC activity. Effective pharmacological agents useful in diagnosis or CC treatment of disease are also identified using APO4 polypeptides/active fragments and APO4 signal transducer molecules that specifically interact CC with a cytoplasmic domain of APO4 and detecting a change in level of APO4 activity. The method is performed in vivo or in vitro. APO polypeptides are all useful as immunogens for preparing antibodies. APO4 is also CC useful for diagnosis/treatment of developmental or gestational CC abnormalities. APO8 was transfected to human breast carcinoma cell line MCF-7, and induced apoptosis.
                                                                                                                                                                                                                                  Sequence 1030
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Browning
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                          (BIOJ ) BIOGEN INC. (UYGE-) UNIV GENEVA FACULTY MEDICINE
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ligand (TRELL). TRELL or active fragments can be included with a
carrier in pharmaceutical compositions to treat cancer, autoimmune
diseases or immune responses to tissue grafts, or to stimulate or
suppress the immune system. It is useful to screen for TRELL
receptors, by labelling with a detectable label and screening
compositions for binding. Agents interfering with TRELL-receptor
binding can also be screened for, can then be administered,
optionally with interferon- gamma, to induce cell death or
treat, suppress or alter immune responses (especially involving human
adenocarcinoma cells) involving a signal pathway between TRELL and its
receptor. The DNA sequence can be used in gene therapy for
TRELL-related disorders in mammals (especially humans), e.g. tumours,
autoimmune and inflammatory diseases or inherited genetic disorders,
by introducing into cells, and expressing, therapeutically effective
amounts of a vector, e.g. a virus comprising a gene encoding TRELL.
It may also be of use in the preparation of prepare probes for
soreening natural/synthetic DNAs for TRELL-encoding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumour necrosis factor related ligand - cancer, auto-immune disease and immune r
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ValLeuAlaLeuArgCysLeuGluGluPheSerAlaThrAlaAlaSerSerLeuGlyPro
                                           CAGGTGCACTTTGATGAGGGAAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGAACGGT
                                                               GlnValHisPheAspGluGlyLysAlaValTyrLeuLysLeuAspLeuLeuValAspGly
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This invention describes isolated Tumor Necrosis Factor (TNF) family receptor polypeptides: APO4, APO6, APO8 and APO9 or their active CC fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or their active fragments. APO4 is useful for diagnosing prostate cancer by determining levels of APO4 in an individual. Prostate cancer can also be treated using APO4 selective binding agents linked to a therapeutic molety. APO4 polypeptides are also useful for identifying selective binding agents, useful in diagnosis/treatment of disease by binding of agents to the polypeptide/active fragment which is extracellular, or expressed on the cell surface. The binding is preferably performed in Vivo. APO4 polypeptides/ active fragments are also useful for screening consists and antagonists by binding and observing the changer in APO4 activity. Effective pharmacological agents useful in diagnosis or treatment of disease are also identified using APO4 polypeptides/active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4 developmental abnormalitty; gestational abnormalitity; prostate cancer; APO6, APO8, APO9, TNRL-I; TNRL-3; diagnosis; treatment; therapy; disea cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
                                                                                                                                                                                                                                     developmental or gestational abnormalities
                                                                                                                                                                                                                                                       New Tumor Necrosis Factor family receptor polypeptides and useful for diagnosis and treatment of prostate cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apoptosis;
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 Homo sapiens BARD1 exon 1.
                        28-SEP-1998
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|CAGGATGTGGTACCTTTCTTGGAACAACTAGTCCGGCCTCGAAGAAGTGCTCCTAAAGGC 180
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CC The sequence is that of containing a BARD1 exon which can be used in the CC preparation of the recombinant breast cancer antigen, BRCA1, binding CC proteins BARD1, B123, BE2, BE14, BE31 or BE445, or a composition for the CC detection of a BARD1, B123, BE2, BE14, BE31 or BE445 nucleic acid CC sequence, specifically a wild type BARD1 composition for the detection CC or purification of BRCA1, useful to identify a patient having, or at CC risk of developing cancer. BARD1 can be used in the preparation of an CC anti-BARD1 antibody, and in the detection and purification of a BRCA1 protein. BARD1, B123, BE2, BE14, BE31 or BE445 can used in the CC identification of a binding protein agonist or antagonist that alters CC the binding of BARD1, B123, BE2, BE14, BE31 or BE445 to BRCA1 or the CC biological activity of the BRCA1-BARD1, B123, BE2, BE14, BE31 or BE445 can used in the CC complex. The antibodies can be used to detect BARD1, B123, BE2, BE14, CC BE31 or BE445, a specific anti-BARD1 antibody can be used to identify CC a patient having or at risk of developing cancer.
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                           GCGGGCCGCCCGGAGACCCTCTAAATTAGAAGCAGCTGCCACTCTAAGTTAAACTGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                 euArgProGlySerSerLeuArgIleArgThrLeuPro----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATCCCGGTCGCGCCTCCAGAGTTTGAATCGGGCTGGGGGTGGGGCCTGAGGCTTCTGCATT
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O-acyltransferase;
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                                                                                                                                acyltransferase gene
                                                                                                   phytosterol;
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a putative coding sequence for a corn lecithin:cholesterol acyltransferase (also known as phosphatidylcholine-sterol O-acyltransferase). This enzyme is found associated with high-density lipoproteins and Apolipoprotein-Al and -D. The gene and protein can be used to produce transgenic plants which have increased lipid metabolism and membrane fluidity, and therefore increased resistance to heat and/or cold shock, to alter the content of phytosterol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide encoding plant lecithin:cholesterol acyltransferase enzyme useful for producing transgenic plants and for producing antibodies specific to which is useful for screening cDNA expression libraries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cahoon
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DB; AAB01210.
                                                                                                                                                                                                                                                                                                                                                            CAACGAGTACCGGAACCTCGCCGG------CGTCGAGACGCGAGTGCCCAACTTCGGCTC
                                                                                                                                                                                                                                                                                                                                                                             ArgArgLeuProLeuProArgSerLeuGlySerArgAspGlyGlyAlaVal-------
CATCCTCGGCCACAGCTTCGGCGCGCATGGTCGCGCTCGAGTTCGTCCGGAACACTCCGCC
                              AspProAlaProPheLeuAsnArg----
                                                                                                                                                                              CTTCCGCTACGCGCCGCCGTCCCCGGCCAGACGTCCGAGGTGTACTCCCGCTACTTCAA
                                                                                                                                                                                                          LeuGlyLeuGlyLeuAlaLeu-----
                                                                                                                                                                                                                                         AGCCGCACTGGAAGACATGGGATACCGAGACGGAGACACCATGTTCGGAGCCCCCTACGA
                                                                                                                                                                                                                                                                                                   CACAAGAGCCTTCAGCCACAAGAACCCCCTCAAGTCAGACTGGTGCCTCGGAAAGCTGAG
                                                                                     LeuValAlaGluGluAspGlnAspProSerGluLeuAsnProGlnThrGluGluSerGln
                                                                                                                    GGAGCTGATGGAGCTGGTCGA-----
                                                                                                                                                AlaValValSerLeuGlySerArgAlaSerLeuSerAlaGlnGluProAlaGlnGluGlu
                                                                                                                                                                                                                                                                   ArgArgArgGlyArgArgGlyGluProGlyThrAlaLeuLeuVal-----ProLeuAla
                                                                                                                                                                                                                                                                                                                            ---ArgGlnAlaGlnProProAlaPro------MetAlaAlaArgArgSerGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 43-44; 49pp; English.
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                                                           - GGCCGCGAGCGAGAGGACCCG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "lecithin:cholesterol acyltransferase"
/EC_number= "2.3.1.43"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1099
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P-PSDB; AAW81525
                           WPI; 1999-024042/02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This CDNA sequence codes for murine JNK-interacting protein 1 (JIP-1, see AAW61625), a novel cytoplasmic anchor protein that specifically binds to and inhibits the biological effects of JNK (C-Jun NH2-terminal kinase), including the initiation of apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c-Jun NH2-terminal kinase (JNK)-interacting protein {\bf 1} - used to treat neurodegenerative disease, blood clot, leukaemia, autoimmu disease, and inflammation
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                                                sequence operatively linked to a polynucleotide sequence encoding an antigen which is a fragment of a gene or genome associated with an infectious disease, cancer and autoimmune disease such as rheumatoid arthritis, vasculitis, and multiple sclerosis, pathogenic genomes consisting of bacterium, fungus, protozoa and virus such as human immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis C virus (HCV), influenza and respiratory syncytial virus (RSV), and optionally comprising a nucleotide sequence encoding a cytokine expression vector), is useful for inducing an immune response (systemic and/or mucosal) in an organism. The cytokine expression vector
                                                                                                                                                                                                                                                                                                                                                     bound to an aggregated protein polycationic polymer conjugate or suspension. The expression vector contains a promoter polynucleotide
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r interleukin-12 (IL-12). The polynucleotide sequences encodin
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2003, 07:42:57; Search time 15.0648 Seconds

(without alignments)
781.906 Million cell updates/sec

Title: Perfect score: US-09-245-198A-4 1444 1 MSLLDFEISARRI.DI

BLOSUM62 Gapop 10.0 , Gapext 0.5

Sequence: MSLLDFEISARRLPLPRSLG......PWAHLKAAPFLTYFGLFQVH 284

Scoring table:

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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-i- SUBUNIT: HOMOTRIMER (POTENTIAL)i- SUBCELLULAR LOCATION: Type II membrane protein and secretedi- TISSUE SPECIFICITY: Highly expressed in adult heart, pancreas, skeletal muscle, brain, colon, small intestine, lung, ovary, prostate, spleen, lymph node, appendix and peripheral blood lymphocytes. Low expression in kidney, testis, liver, placenta, thymus and bone marrow. Also detected in fetal kidney, liver, lung and braini- pTM: The soluble form derives from the membrane form	PUNECTION. PUDMEd=10085077; Lynch C.N., Wang Y.C., Lund J.K., Chen YW., Leal J.A., Wiley S.R.; Lynch C.N., Wang Y.C., Lund J.K., Chen YW., Leal J.A., Wiley S.R.; Lynch C.N., Wang Y.C., Lund J.K., Chen YW., Leal J.A., Wiley S.R.; "TWEAK induces angiogenesis and profit profit cells."; J. Biol. Chem. 274:8455-8459(1999). -i- FUNCTION: Binds to FN14 and possibly also to TNRFSF12/APO3. Weak inducer of apoptosis in some cell types. Mediates NF-KappaB activation. May promote angiogenesis and the proliferation of endothelial cells.	. for	I.A., AND N-TERMINUS OF and Fetal liver; S. pubMed=9405449; Y., Bourdon P.R., Xu H. Cia I., Browning J.L.; ecreted ligand in the apoptosis."; 272:32401-32410(1997). I.A. I.A. dney; 5; PubMed=9560343;	F

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                        TN12_MOUSE
O54907; O9CTP2;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last sequence)
                                                                                                                                                                    MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a linear removed.
   Eukaryota;
                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SITE
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Pfam; PF00229; TNF; 1.
SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                        241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by proteolytic processing.
SIMILARITY: BELONGS TO THE TUMO!
CAUTION: Ref. 3 sequence differs
                                                                                                                                                                                                                                      TYFGLFQVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        frameshift in position 125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQD 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602695; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                       TYFGLFQVH
                                                                                                                                                                                                                                                                                                                      LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL 275
                                                                                                                                                                                                                                                                                                                                                                                         GAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLD
                                                                                                                                                                                                                                                                                                       LLVDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF055872; AAC39724.1; -.
BC019047; AAH19047.1; ALT_FRAME
; HGNC:11927; TNFSF12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOZU; A...,
PS00251; TNE_1; FALSE_NEG.
PS50049; TNE_2; 1.
PS50049; Transmembrane; Glycoprotein; Signal-anchor.
PS50049; Transmembrane; Glycoprotein; Signal-anchor.
TUMOR NECROSIS FACTOR LIGARD SUPERFAMILY
TUMOR NECROSIS FACTOR CHARLES OF SUPERFAMILY
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93
139
249
 Metazoa;
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BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
f.3 sequence differs from that shown due to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139
27216
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94
 Chordata;
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42
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100.0%;
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N-LINKED (GLCNAC. . .).
; E660843361C28EBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1268; DB 1; Length 249; Pred. No. 2e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 12, SECRETED FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
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Craniata;
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Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                  12 (TNF-related weak
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 Euteleostomi;
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   DOMAIN
                                                                                                                 CHAIN
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                                                                                  CHAIN
                                                  TRANSMEM
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Genriboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Ra Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashtaki P., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                      SMART; SMUVAV,
PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
PROSITE; PS50049; TNF_2; 1.
PROSITE; PS50049; Transmembrane; Glycoprotein; Signal-anchor.
PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:1196259; Tnfsf12.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit modified and this st entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
-i- FUNCTION: Binds to FN14 and possibly also to TNRFSF12/APO3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Peritoneal macrophage;
MEDLINE=98070415; PubMed=9405449;
Chicheportiche Y., Bourdon P.R., Xu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
NCBI_TaxID=10090;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF030100; AAC53517.1; -. EMBL; AK020909; BAB32249.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kawai J.,
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"TWERK, a new secreted ligand in the tumor necrosis factor family that weakly induces aportrosis".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Binds to FN14 and possibly also to TNRFSF12/APO3. Weak inducer of apoptosis in some cell types. Promotes anglogenesis are the proliferation of endothelial cells. Mediates NF-KappaB activation (By similarity).

SUBUNIT: Homotrimer (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: The soluble form is produced from the membrane for proteolytic processing (By similarity).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity).
TISSUE SPECIFICITY: WIDELY EXPRESSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-profit institutions as long as its content and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shinagawa A., Shibata K.,
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272:32401-32410(1997).
                                                                                                                                                      225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                         MEMBER 12, SEC SIGNAL-ANCHOR
                                                                                                                                                  MEMBER 12, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
                               EXTRACELLULAR (POTENTIAL)
                                                               (POTENTIAL)
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(See http://www.isb-sib.ch/announce/
(BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSu
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                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                  SUPERFAMILY
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RESULT
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                                                                                                                                                                                                                                        A Tregaskes C.A., Young J.R., Burnside J.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
C -!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulic c class switching (By similarity).
C -!- SUBUNIT: Homotrimer (By similarity).
C -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists a extracellular soluble form (By similarity).
C -!- PIM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
C -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         L) (CD154 protein).
L) (CD154 protein).
TNFSF5 OR CD40LG OR CD40L.
Gallus (Chicken).
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID CARBOHYD
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                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member
                         InterPro; IPR003636; TNF_abc.
InterPro; IPR00478; TNF_family.
Pfam; PF00229; TNF; 1.
ProDom; PD002012; TNF_abc; 1.
                                                                                            EMBL; AJ243435; CAB95748.1; HSSP; P29965; 1ALY.
                                                                                                                                   or send
                                                                                                                                                modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-White leghorn;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9031;
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                                                                            InterPro; IPR003263; TNF_5
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                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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SM00207; TNF;
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115
225
                                                                                                                                   email to license@isb-sib.ch).
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88.8%;
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Mismatches 16
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                                                                                                                                              http://www.isb-sib.ch/announce/
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Submitted (A)
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16-OCT-2001
16-OCT-2001
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CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
SITE
DISULFID
                      or send an email to license@isb-sib.ch).
                                                                         the
                                                                                                   This
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. Hosie M.H., Willett B.J.;
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                  Tumor necrosis factor ligaTNFSF5 OR CD40LG OR CD40L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 RRAIAAHYEVHPRPGQDGAQAGVDGTVSGW-EEARINSSSPLRYNRQIGEFIVTRAGLYY 197
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                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EWBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ittes requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                      PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                     juvant properties of canine CD40L."; mitted (AUG-1998) to the EMBL/GenBank/DDBJ databases. FUNCTION: Cytokine that binds to TWERSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as Igl production in the presence of IL-4. Involved in immunoglob class switching (By similarity).
                                                                                                                                                            SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
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AF086711; AAD04375
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42; Conserv
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PS50049;
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el. 41, Last annotation update)
factor ligand superfamily member
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TNF_2;
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44
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Glycoprotein;
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N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
5409F24A8E53CCD7 CRC64;
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; ; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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Canis.
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Best Local
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P41273;
O1-FEB-1995
O1-FEB-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID CARBOHYD
                                                                                                 SEQUENCE FROM N.A.
MEDLINE-94374434; PubMed-8088337;
Alderson M.R., Smith C.A., Tough T.W., Davi
Falk B., Roux E., Baker E., Sutherland G.R.
"Molecular and biological characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPRO03636; TNF_abc.
Interpro; IPRO03636; TNF_family.
Pfam; PF00229; TNF; 1.
Prodom: Process
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                             Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD008600; TNS; SMART; SM00207; TNF;
                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                       1BBL)
                                                                                                                                                                                                                               Tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                     233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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proliferation of activated peripheral blood T cells. May have role in activation induced cell death (AICD). May play a role cognate interactions between T cells and B cells/macrophages. SUBUNIT: HOMOTRIMER (POTENTIAL).
SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                                                 GSSLRIRTLPWAHLKAAPFLTYFGLFQV 283
                                                                                                                                                                                                                                                                                                                                                                                                                               YEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFD::| | | | | | | | | | |
                                                                                                                                                                                                                                                                                                                                    GASVFVNVTDPSQVSHGTGFTSFGLLKL
                                                                                                                                                                                                                                                                                                                                                                              SNRAASSQAPF
                                                                                                                                                                                                                                                                                                                                                                                                EGKAVYLKLDLLVDGVLALRCLEEFSAT - - - - - AASSLGPQLRLCQVS - - -
                                                                                                                                                                                                                                                                                                                                                                                                                    EMKKEENIAMQKGDQDPRIAAHVISEASSNPASVL-----RWAPKGYYTISSNLVSL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EPAQEELVAEE--DQDPS-ELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAH 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00251; TNF_1; 1.
PS50049; TNF_2; 1.
Pransmembrane; GI
                                                                                                                                                                             Eutheria;
                                                                                                                                                                                       Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47
111
177
177
239
260
                                                                                                                                                                                                                             (Rel. 31, Created)
(Rel. 31, Last sequence update)
(Rel. 41, Last annotation update)
sis factor ligand superfamily member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                  STANDARD;
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Primates;
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46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal-anchor.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TUMOR NECROSIS FACTOR LIGAND MEMBER 5, SOLUBLE FORM (BY SI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLEAVAGE (BY SIMILARITY).
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                                                                                                                                                                           Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LINKED (GLCNAC. . .) (P 604F69A19E98EB70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                  , Davis-Smith T., add G.R., Din W.S., of ation of human 4-11
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                                                                                                                                                                           Vertebrata;
i; Hominidae;
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                                                                                                     4-1BB
                                                                                                                                                                                      Euteleostomi;
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Goodwin R.
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role
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RESULT CG22_AN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
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Best Local S
Matches 74
                                                                                                                                                                                                                                    _ANTMA CG22_ANTMA STANDARD; PRT; 441 AA P34801;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
62/mitotic-specific cyclin 2
Fobert P.R., Coen E.S., Murphy G.J.P., "Patterns of cell division revealed by genes during the cell cycle in plants."
                                                                                                                                                   Antirrhinum majus (Garden snapdragon).
Eukaryota; Viridiplantae; Streptophyta; Embryc
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; euasterids I; Lamiales; Veronicace;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
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                                                                 SEQUENCE FROM N.A. MEDLINE=94148008; Pubmed=8313906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                NCBI_TaxID=4151;
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                      Doonan J.H.;
transcriptional regulation
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Best Loc
Matches
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PIR; S41710; S4
"SSP; P30274; 7
TPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                             Macropus eugenii (Tammar wallaby).
Eukaryota; Metazoa; Chordata; Crania
Mammalia; Metatheria; Diprotodontia;
                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis factor ligand superfamily member 1)
LTA OR TNESE1 OR TNFB.
                                                                                                                                                                                                   Q9XT48;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00292; CYCLINS; 1.
Cyclin; Cell cycle; Cell division; Mitosis.
SEQUENCE 441 AA; 49205 MW; E6E4C037C98880A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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SEQUENCE FROM N.A.
MEDLINE-20284948; PubMed-10826697;
                                                 NCBI_TaxID=9315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR004366; Cyclin.
InterPro; IPR004367; Cyclin_Cterm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G2/M (MITOSIS) TRANSITION. G2/M CYCLINS ACCUMULATE STEADILY DURING G2 AND ARE ABRUPTLY DESTROYED AT MITOSIS.

SUBUNIT: INTERACTS WITH THE CDC2 AND CDK2 PROTEIN KINASES TO FORM A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.

DEVELOPMENTAL STAGE: ACCUMULATES STEADILY DURING G2 AND IS ABRUPTLY DESTROYED AT MITOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN AB SUBFAMILY.
                                                                                                                                                                                                                                                                                                                      TIN-IVDRYLASKTTSRRELQLLGMSSMLIASKYEEIWAPEVNDLVCISDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAVRQAQPPAPMAARRSQRR-------RGRRGEPGTALLVPLALGLGLALACLGLL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. 13:616-624(1994)
                                                                                                                                                                                                                                                                                                                                                         KLDLLVDGVLALRC----
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                                                                                                                                                                                                                                                                                                                                                                                                                            SGWEE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                            --APVLEKEITGEKSLKKKAPTLTSTLTARSKAASV-VRTKPKEQIVDIDAADVNNDLAV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPAPFLNRLVRPRRS----APKGRKTRARRAIAAHYEVHPRPGQ-----DGAQAGVDGTV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANAEAAAAENNKNSLAVNAKGADGALPIKRAVARVPVQKKTVKSKPQEIIEISPDTEKKK 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00134; cyclin; 1.
PF02984; cyclin_C; 1.
SM00385; CYCLIN; 2.
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                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                       -LEEFSATAASSLGPQLRLCQVSGLLALRPGS
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Pred. No. 1.6;
4; Mismatches 104;
                                                                                  Craniata; Vertebrata;
                                                                                                                                                                                                                                      PRT;
                                                                  Macropodidae;
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1.6;
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                                                                 Macropus
                                                                                  Euteleostomi;
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Query Match
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00251; TNE_1; 1.

PROSITE; PS50049; TNE_2; 1.

Cytokine; Glycoprotein; Cytotoxin; Signal.

SIGNAL 1 27

CHAIN 28 201

CARBOHYD 93 93

N-LINKED (GLCN
SEQUENCE 201 AA; 21536 MW; 8C4C371CB509
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DNA Seg. 10:399-403(2000).
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InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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between the
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FUNCTION: Cytokine that in its homotrimeric form binds to THERSFIA/THERI, THERSFIB/THEBR and THERSFIA/HVEM. In its heterotrimeric form with LTB binds to THERSF3/LTBR. Lymphotoxin produced by lymphocytes and cytotoxic for a wide range of tumor
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SUBUNIT: Homotrimer, and heterotrimer of
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ween the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVLLFSSKYQVHVPLLSAQKSVCSGTQGPWMRSVYQGAVFLLTQGDRLSTYTDGVSHLLQ
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                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.68;
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Last annotation
ligand superfam
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nnotation update)
superfamily member
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Pred. No. 0.
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                                                                                             (Cynomolgus
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                                                                                                 monkey),
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Query Match
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Mammalia; Eutheri
Cercopithecinae;
NCBI_TaxID=9544,
                                                                   CARBOHYD
                                                                                                                            DISULFID CARBOHYD
                                                                                                                                                                    DOMAIN
DOMAIN
SITE
                                                SEQUENCE
                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF344856; AAK37539.1; -.
EMBL; AB035138; BAA90294.1; -.
EMBL; AB035139; BAA90295.1; -.
EMBL; AB035140; BAA90296.1; -.
HSSP; P01375; 4TSV.
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                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Willinger F., Bostik P., Mayne A.E., King C.L., Weiss W.R., Ansari A.A.; "Cloning, sequencing, and homology analysis of Fas/Fas-ligand and co-stimulatory molecules.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01234; TNECROSISFCT ProDom; PD002012; TNF_abc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                 Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES-M.mulatta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-M.mulatta; TISSUE-Lymphocytes;
MEDLINE-21383618; PubMed-11491535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type II me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3 modulates its effects (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nitted (NOV-1999) to the EMBL/GenBank/DDBJ databases FUNCTION: Cytokine that binds to TNFRSF6/FAS, a rec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00229; TNF;
                                                                                                                                                                                                                                                                                                                                                       PS50049; TNE_2; 1.

PS50049; TNE_2; 1.

PS50049; Signal-anchor.

PS50049; Signal-anchor.

PS50049; Signal-anchor.

PS50049; Signal-anchor.

PS50049; Signal-anchor.

PS50049; Signal-anchor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inoue T.
                                                280
                                                                                                                            445
128
201
183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TNE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macaca
9541,
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                                                                                    280
69
64
129
232
232
249
259
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101
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        50
                                                MW.
      Score
                                                                 N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
S -> P (IN REF. 1).
                                                                                                                                                 POTENTIAL.
                                                                                                                                                                CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                               EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                     SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                              CYTOPLASMIC
                                                                                                                                                                                                                                                                                                               TUMOR NECROSIS FACTOR LIGAND MEMBER 6, SOLUBLE FORM (BY S.
                                                                                                                                                                                         POLY-PRO.
                                                                                                                                                                                                              PRO-RICH
                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Cercopithecidae;
                                            F0B284D61A132EB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               membrane protein and secreted
      94;
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    DB
                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.L.,
  1;
Length 280;
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                                            CRC64;
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                                                                                  (POTENTIAL)
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RESULT 9
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Matches 62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHO_MICLU
P52154;
01-OCT-1996
              use by modified
entities
                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                  Opperman T., Richardson J.P., "Phylogenetic analysis of sequences f homology to the Escherichia coli rho
                                                                                                                                                                                                                                                                                                                                                                                                             Nowatzke W.L., Richardson J.P.;
"Characterization of an unusual Rho factor from the high G + C positive bacterium Micrococcus luteus.";
J. Biol. Chem. 271:742-747(1996).
                                           the European Bioinformatics Institute.
                                                                                                                                                                                                                Submitted
-!- FUNCT!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Actinobacteria; Actinobacteria (class); Actinomycetales; Micrococcineae; Micrococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                            Nowatzke W.L.;
                                                                                                                                                                                                                                                            STRAIN-EM
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 205-690 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-96132802; PubMed-8557681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription termination
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94327472; PubMed=8051015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Micrococcus luteus (Micrococcus lysodeikticus)
                                                                                                                                                                                                                                                                          REVISION TO
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                                                                                                                                                                                                                                                                                                       Bacteriol.
                                                                                          SUBUNIT: HOMOHEXAMER (BY SIMILARITY).
SIMILARITY: CONTAINS 1 RNA RECOGNITION MOTIF (RRM).
                                                                                                                                                RNA-DEPENDENT ATPASE ACTIVITY, AND RELEASE OF THE MRNA FROM DNA TEMPLATE. RNA-DEPENDENT NTPASE WHICH UTILIZES ALL FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS WELL AS DATP AS SUBSTRATES,
                                                                                                                                                                                            nitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
FUNCTION: FACILITATES TRANSCRIPTION TERMINATION BY A MECHANISM THAT INVOLVES RHO BINDING TO THE NASCENT RNA, ACTIVATION OF RH
                                                                                                                                    HAS A SIGNIFICANT LOWER ACTIVITY WITH CTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEA-RINSSSPLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTGQMWAHSSYLGAVFNLTSADHLY-----VNVSELSLVNFEESQ--TFFGLYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNROIGEFIVTRAGLYYLYCOVHFDEGKA-----VYLKLD-----LLVDGVLALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QIGHP---SPPPEKKEQRK--VAHLTGKPNSRSMPLE-----WEDTYGIVLLSGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLN 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQV
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            non-profit institutions as long and this statement is not removed.
requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                          500.
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Q11162;
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                        SEQUENCE FROM N.A.

STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Whi

Fleischmann R.D., BeBoy R., Dodson R., Gwinn M.L., Haft D., Hic

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Ermolaeva M.D., Sa

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Sa

Belcher A., Utterback T., Weldman J., Khouri H., Gill J.,
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01-OCT-1996 (Rel. 34, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein Rv0497.
RV0497 OR MT0517 OR MTCY20G9.23.
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Actinomycetales; Corynebac
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InterPro; IPR002059; Cold_shock.
InterPro; IPR004665; Term_rho.
Pfam; PF00006; ATP-synt_ab; 1.
SMART; SM00357; CSP; 1.
TIGREAMS; TIGR00767; rho; 1.
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                                                Bishai W.;
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    laboratory strains.";
                        *Whole genome comparison
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RNA-BINDING (RNP1)
ATP (POTENTIAL).
G -> P (IN REF. 2; I
F77C4C75EE1B8998 (
                        Mycobacterium tuberculosis
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t D., Hickey E.,
M.D., Salzberg
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PRT: 24(
043557; 075476; 096LD2; 098VF8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence upda
15-JUN-2002 (Rel. 41, Last annotation up
Tumor necrosis factor ligand superfamil)
mediator-ligand) (HVEM-L).
TNFSF14 OR LIGHT OR HVEML.
Mauri D.N., Ebner R., Montgomery R.I., Ko
Yu G.-L., Ruben S., Murphy M., Eisenberg
Ware C.F.;
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                                 SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=98122340; PubMed=9462508;
                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; C
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                                                                               Mammalia;
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                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                   GALVVLQSILAVAFGAGLF-----IAFDQLWRWNSIVALVLSVMVILGLVVSVRAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-profit institutions as long and this statement is not removed.
                                                                              Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 protein;
231 251
257 277
286 30;
33 3
197 20
310 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.48; llarity 24.48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rv0497;
                                                                                                                                                                                                                                                                                                                                                                       -EVHPRPGQDG-----AQAGVDGTVSGWEEARINSSS----PLRYN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
277
306
39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202
33092
                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 93; Pred. No.
                                                                                                                                    nnotation update) superfamily member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-ARG.
POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ----VQVGEAAPQSPAEPVAEQ-VAEEPTRTVYWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                               Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4954027F694DF5C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                            246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              membrane
                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete
                                                                                                                                                                                                240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
          Kochel K.D., Cheung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ormatics and the EMBL outs
There are no restrictions
ong as its content is in
                                                                                          Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                               B
                                                                               Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64
                                                                                                                                      14
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                                                                                                                                     (Herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by
                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310;
                                                                                                                                                                                                                                                                                                                         -LVDGVLALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120;
          T.C.,
Spear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                     entry
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EMBL;
EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                response locus on chromosome 19p13.3 and distinct isoforms gener by alternate splicing or proteolysis.";
J. Immunol. 167:5122-5128(2001).
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. use by non-profit institutions as 10 modified and this statement is not remo
                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Herpesvirus entry mediator ligand HVEM/TR2, stimulates proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha ligands for herpesvirus entry mediator."; Immunity 8:21-30(1998).
                                           SMART; SM00207; TNF;
                                                              ProDom;
                                                                                                        InterPro; IPR003636; TNF_abc
InterPro; IPR000478; TNF_fam
                                                                                                                                                                               Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Truneh A., Young P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DiPrinzio R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tan K.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-98438532; PubMed-9765287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORM 1),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION PTM: N-glycosylated.
PTM: The soluble form of isoform 1 derives from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTERNATIVE ROCCULOR OF ALTERNATIVE SPLEEN BUT ALSO TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN PERIPHERAL LYMPHOID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the decoy receptor TNFRSF6B modulates its effects. Activates NFKB, stimulates the proliferation of T cells, and inhibits growth o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          form by proteolytic processing.
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (isoform 1); Cytoplasmic (isoform 2).
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 frameshift in position 178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND NO EXPRESSION SEEN IN FETAL TISSUES, NONHEMATOPOIETIC TUMOR LINES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMITISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Type II membrane protein and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: Homotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                  AF036581; AAC39563.1; -. AF064090; AAC25169.1; -. AY028261; AAK26160.1; -. BC018058; AAH18058.1; AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J., B., Dede K., Spampanato J., Silverman C., Hensley P., zio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
                                                                                                                                                                           HGNC:11930; TNFSF14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adenocarcinoma HT-29. Acts as a receptor for Herpes simplex
PS00251;
PS50049;
                                                                                                                                                                                                                                                                                                                                                                                                                                         the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ref. 4 sequence differs from that shown
                                                                                                                                                                                                  4TSV.
                                                                                     TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273:27548-27556(1998).
TNF_1; FALSE_NEG TNF_2; 1.
                                                            TNF_abc; 1
                                                                                                        TNF_family
                                                                                                                                                                                                                    ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                  is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HVEM-L), a novel ligand of T cells and inhibits I
                                                                                                                                                                                                                                                                                                                                                                                                    long
                                                                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                       There are
                                                                                                                                                                                                                                                                                                                                                                                                    as its content
                                                                                                                                                                                                                                                                                                                                                                             Usage
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                                                                                                                                                                                                                                                                                                                                                                               and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               generated
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RESULT 12
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Best Local
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VARSPLIC
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        CERTO
                                                                                                                                      Weiss W.R., Ansari A.A.;
"Cloning, sequencing and Factor.
                                                                                                                                                                TISSUE-Lymphocytes;
MEDLINE-21383618; PubMed-11491535;
Villinger F., Bostik P., Mayne A.E
                                                                                                                                                                                                                                                      Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SITE
          -!- SUBUNIT: Homotrimer (Probable).
-!- SUBCELLULAR LOCATION: Type II membrane
                                                                                                                  *Cloning, sequencing, and homology analysis Fas/Fas-ligand and co-stimulatory molecules Immunogenetics 53:315-328(2001)
                                                                                                                                                                                                                                                                                          TNESF6 OR FASL OR CD95L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            Cercopithecinae; Cercocebus.
                                                                                                                                                                                                                                                                                                                                                               Q9BDN1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytokine;
                                                                                                                                                                                                                              NCBI_TaxID=9531;
                                                                                                                                                                                                                                                                                                                                                                             TNF6
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                                                                                                                                                                                                                                                                                                                                                                                                                                        142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
                              transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3 modulates its effects (By similarity).
                                                                                                      FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                       YIYSKV 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLYCQV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQI-----
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                                                                                                                                                                                                                                                                                                                                                                            CERTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 23.7
44; Conservative
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58
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23.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SGGPLLWETQLGLAFLRGLSYHDGALVVTKAGYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRLPDGPAGSWEQLIQERRS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 92;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L -> V (IN REF. 4).
E -> K (IN REF. 2).
; 49D0BF67E1390B39 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEMBER 14, SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISSING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEMBER 14, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED
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                                                                                                                                                                    King C.L.,
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            protein
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                                                                                                                                             nonhuman
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            (B)
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NFC4_HUMAN
                                                                                                                                                                        RESULT 13
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Matches
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PROSITE; PS000251; TNF.1; 1.

PROSITE; PS50049; TNF.2; 1.

Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

MEMBER 6, SOLUBLE FORM (BY SIMILARITY).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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CARBOHYD
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CARBOHYD
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                         16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01234; TNECROSISFCT ProDom; PD002012; TNF_abc; 1. SMART; SM00207; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (Some or send an email to license@isb-sib.ch).
                                                                                                   NFC4_HUMAN
Q14934;
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     Nuclear
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InterPro; IPR000478;
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SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                CTTGQMWAHSSYLGAVFNLTSTDHLY-----VNVSELSLVNFEESQ--TFFGLYKL
                                                                                                                                                                                                                                                                                              CLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIRTLPWAHLKAAPFLTYFGLFQV
                                                                                                                                                                                                                                                                                                                                                                                               YNRQIGEFIVTRAGLYYLYCQVHFDEGKA------VYLKLD------LLVDGVLALR 225
                                                                                                                                                                                                                                                                                                                                                                                                                                               QIGHP---SPPPEKKEQRK--VAHLTGKPNSRSMPLE-----WEDTYGIVLLSGVK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLN 121
                                                                                                                                                                                                                                                                                                                                                 YKK--GGLVINETGLYFVYSKVYF-RGQSCTNLPLSHKVYMRNSKYPQDLVMMEGKMMSY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEA-RINSSSPLR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLCLLVMFFMVLVALVGLG--LGMFQLFHLQKEL------AELRESTSQKHTASSLEK 128
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  activated T-cells, cytoplasmic 4 (T
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TNF_family.
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               Created)
Last sequence update)
Last annotation update)
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Pred. No.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
729EA60067B7D398 CRC64;
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                                                                                                                                                                                                                                                                                                283
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     TIPE TO COLUMN TERROR DE LA PRESENTA DE LA PRESENTA DE LA COLUCIO COLUMNA COLUMNA EL PRESENTA DE LA PRESENTA DEL PRESENTA DE LA PRESENTA DE LA PRESENTA DE LA PRESENTA DEL PRESENTA DE LA PRESENTA DEL PRESENTA DEL PRESENTA DEL PRESENTA DE LA PRESENTA DEL PRESENTA DE LA PRESENTA DEL 
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between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoey T., Sun Y.-L., Williamson K., Xu X.;
"Isolation of two new members of the NF-AT gene family and characterization of the NF-AT proteins.";
Immunity 2:461-472(1995).
                                                REPEAT
DOMAIN
                                                                                                                        DOMAIN
                                                                                                                                                                        Repeat;
                                                                                                                                                                                                                                                                                        InterPro; IPR002909; IPT_TIG.
InterPro; IPR000451; NF_Rel_dor_fam
Pfam; PF01833; TIG; 1.
SMART; SM00429; IPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                               MIM; 602699;
                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:7778; NFATC4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
REVIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=95269130; PubMed=7749981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606
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                                                                                                   REPEAT
                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                         Transcription regulation;
                                                                                                                                                                                                                                                PROSITE; PS01204; REL_1; PROSITE; PS50254; REL_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSFAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L41066; AAA79175.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: PLAYS A GENES IN T CELLS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell 96:611-614(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 (BY SIMILARITY).

4 (BY SIMILARITY).

5 SUBUNIT: MEMBER OF THE MULTICOMPONENT NEATC TRANSCRIPTION COMPLETION THAT CONSISTS OF AT LEAST TWO COMPONENTS, A PRE-EXISTING CYTOPLASMIC COMPONENT NEATC2 AND AN INDUCIBLE NUCLEAR COMPONENT NEATC2. OTHER MEMBERS SUCH AS NEATC4, NEATC3 OR MEMBERS OF THE NEATC1. OTHER MEMBERS SUCH AS NEATC4, NEATC3 OR MEMBERS OF THE NEATC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO BE ONE MECHANISM BY WHICH CELLS DISTINGUISH BETWEEN SUSTAINE AND TRANSIENT CALCIUM SIGNALS. THE SUBCELLULAR LOCALIZATION OF NEATC PLAY A KEY ROLE IN THE GENE TRANSCRIPTION.

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN PLACENTA, LUNG, KIDNEY, TESTIS AND OVARY. WEAKLY EXPRESSED IN SPLEEN AND THYMUS. NOT EXPRESSED IN PERIPHERAL BLOOD LYMPHOCYTES.

DOMAIN: REL SIMILARITY DOMAIN (RSD) ALLOWS DNA-BINDING AND COOPERATIVE INTERRACTIONS WITH API FACTORS, USY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACTIVATING PROTEIN-1 FAMILY, MAF, GATA4 AND CBP/300 CAN ALSO BIND THE COMPLEX. NFATC PROTEINS BIND TO DNA AS MONOMERS.
SUBCELLULAR LOCATION: CYTOPLASMIC FOR THE PHOSPHORYLATED FORM AND NUCLEAR AFTER ACTIVATION THAT IS CONTROLLED BY CALCINEURIN-MEDIATED DEPHOSPHORYLATION. RAPID NUCLEAR EXIT OF NFATC IS THOUGHT TO BE ONE MECHANISM BY WHICH CELLS DISTINGUISH BETWEEN SUSTAINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: PHOSPHORYLATED BY NFATC-KINASE; DEPHOSPHORYLATED CALCINEURIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE REL/DORSAL FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                               Phosphorylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ROLE IN THE INDUCIBLE EXPRESSION OF CYTOKINE ESPECIALLY IN THE INDUCTION OF THE IL-2 AND
                                                                                                                                                                                                                                                                       FALSE_NEG
                                                                                                                                                                                                                      Activator; Nuclear protein; DNA-binding;
                                                                                                                        CALCINEURIN-BINDING 2 APPROXIMATE SP REI
                                                   POLY-PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
     DNA-BINDING
                         NUCLEAR LOCALIZATION SIGNAL
                                                                          (APPROXIMATE).
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                                                      EMBL; AF250844; AAF64514.1; -. EMBL; U60872; AAC52672.1; -. EMBL; U59881; AAC52672.1; JOINED EMBL; U59882; AAC52672.1; JOINED EMBL; U59883; AAC52672.1; JOINED EMBL; U59884; AAC52672.1; JOINED EMBL; U59884; AAC52672.1; JOINED HSSP; P23367; 1BKN.
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SEQUENCE
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Mus musculus (Mouse).
Mus musculus (Mouse).
Thervaryota; Metazoa; Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                               modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96270514; PubMed=8674118;
Edelmann W., Cohen P.E., Kane M., Lau K., Morrow I
Umar A., Kunkel T., Cattoretti G., Chaganti R., P.
Kolodner R.D., Kucherlapati R.,
"Meiotic pachytene arrest in MLH1-deficient mice.
"Meiotic pachytene arrest in MLH1-deficient mice.
Cell 85:1125-1134 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kumaran M., Rao M.R.S.; "Cloning of the cDNA of Submitted (MAR-2000) to
                                                                                                                                                                                                                                                                                                                 or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-151 FROM N.A
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SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
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                                   MGI:10]
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                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long
                                                                                                                                                                                                                                                                                                              email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MutL homolog, MLH1 from mouse EMBL/GenBank/DDBJ databases.
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Sciurognathi;
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Matches 70
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  This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01119; DNA_mis_repair; 1.
Pfam; PF02518; HATPase_c; 1.
TIGRPAMS; TIGR00585; mutl; 1.
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE-Skeletal muscle;
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDH15 OR CDH14 OR CDH3.
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SEQUENCE
                                                                                                                                                                                                                                                                      Strausberg R.;
                                                                                                                                                                                                                                                                                                  TISSUE=Muscle;
                                                                                                                                                                                                                                                                                                                                                                       Shibata T., Shimoyana Y., Gotoh M., Hirohashi : "Identification of human cadherin-14, a novel : II cadherin, by protein interaction cloning."; J. Biol. Chem. 272:5236-5240(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97184182; PubMed-9030594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          713
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                                                DIFFERENTIATION.
SUBCELLULAR LOCATION:
SIMILARITY: CONTAINS
                                                                                                                       mitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EUNCTION: CADHERINS ARE CALCIUM DEPENDENT CELL ADHESION PROTEIN THEY PREFERENTIALLY INTERACT WITH THEMSELVES IN A HOMOPHILIC MANNER IN CONNECTING CELLS; CADHERINS MAY THUS CONTRIBUTE TO THE SORTING OF HETEROGENEOUS CELL TYPES, M-CADHERIN IS PART OF THE MYOGENIC PROGRAM AND MAY PROVIDE A TRIGGER FOR TERMINAL MUSCLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRIRTLPW
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     SWISS-PROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SK---
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PF02518; HATPase_c; 1
AMS; TIGR00585; mutl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLEGLPIFILRLATEVNWDEEKECFESLSKECAMFYSIRKQYILEESTLSGQQSDMPGST
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  entry
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Primates;
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22.7%;
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Catarrhini; Hominidae
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No. 9
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) (Cadherin-15)
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  produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
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       collaboration
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Search completed: March 31, 2003, 07:58:06 Job time: 19.0648 secs
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
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InterPro; IPR00023; Cadherin, 5.
Pfam; PP00028; Cadherin, 5.
Pfam; PP01049; Cadherin, C_term; 1.
PRINTS; PR00205; CADHERIN.
SMART; SM00112; CA; 4.
PROSITE; PS00232; CADHERIN_1; 2.
PROSITE; PS00236; CADHERIN_2; 5.
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DOMAIN
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HSSP; P15116; 1NCJ.
Genew; HGNC:1754; CDH15.
MIM; 114019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell adhesion; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D83542; BAA12012.1; -.
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                                                               694 GR-----
                                                                                                                             641 HGPQDDLRDNVLNYDEQGGGEEDQDAYDISQLRHPTALSLPLGPPPL--
                                                                                                                                                                                                                                                      533 SLSQVNVSHARL-RPRHQVPEGLHRLSLLLRDSG-----QPP----QQREQPLNVTVCRC 582
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                                                                                            GRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIGEFI 189
                                                                                                                                                                                                                       GRRGE--PGTALLVPLALGLGLALACLGLLLA------VVSLGSRASLSAQEPAQ--- 92
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                               -----LHPQP-----
                                                                                                                                                                                                                                                                                                                                  6.3%;
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60
814
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CADHERIN 5.
CADHERIN 5.
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N-LINKED (GLCNAC. . .) (POT
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CADHERIN
CADHERIN
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                                                                                                                                                                                                                                                                                                                                  Score 90.5;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MUSCLE-CADHERIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
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                                                               ----PRVLPTSPL----DIADFI 715
                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                  52;
                                                                                                                                                                                                                                                                                                                                               Length 814;
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Run OM protein - nucleic search, using frame_plus_p2n model 9 1: March 31, 2003, 01:56:48 ; Search time 1878.64 Seconds (without alignments)
2448.323 Million cell updates/sec

Scoring table: Perfect score: US-09-245-198A-4 1444 MSLLDFEISARRLPLPRSLG...PWAHLKAAPFLTYFGLFQVH

Title:

BLOSUM62

Searched: Xgapop 10.0, Ygapop 10.0, Fgapop 6.0, Delop 6.0, 16154066 seqs, Xgapext Ygapext Fgapext Delext 8097743376 residues 0.5 0.5 7.0

Minimum DB Maximum DB seq length: 0 seq length: 2000000000

Total number of hits satisfying chosen parameters:

32308132

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Command line parameters:

-MODEL-frame+_p2n.model -DEV=xlh
-O-/cgn2_1/USPTO_spool/US09245198/runat_24032003_163554_25956/app_query.fasta_1.846
-O-/cgn2_1/USPTO_spool/US09245198/runat_24032003_163554_25956/app_query.fasta_1.846
-DB=EST_OFMY=fastap -SUFFIX=rst -MINNATCH+0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-DOCALION=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALION=15 -MODE=LOCAL
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-NO_XLDXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 Database : YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

em_estmu:*
em_estov:* em_gss_hum:*
em_gss_inv:*
em_gss_pln:*
em_gss_vrt:*
em_gss_fun:* gb_est1:* em_estpl: * em_htc:* em_estro:* em_esthum:* em_estin:* em_estba:* em_gss_mam:* gb_gss:* em_estom:* em_estfun:* gb_est5:* gb_est4:* gb_est3:* gb_htc:* gb_est2:* em_gss_mus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C 440 43 38 45 44 45 45 45 45 45 45 45 45 45 45 45	32 33 35 35 37	25 26 27 28 29 29 30 31	114 115 116 117 118 119 119 119 119 119 119 119 119 119	71110 9 8 8 7 7 6 5 5 4 3 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
391 363 363 362 353 353 347 320	441 440 421 420 403 395.5	2	742.53 742.53 646.52 646.55 646.55 598.55 598.55 598.55	1087.5 1060.5 1060.5 979 962 934 913 909.5 825 825 753	. 0
27.1 26.9 25.1 24.4 24.4 22.2	30.5 30.5 29.2 29.1 27.9	38.9 35.0 34.6 33.0 32.3	50 50 50 50 50 50 50 50 50 50 50 50 50 5		Query Match I
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ALIGNMENTS

RESULT 1 BI871711 LOCUS

DEFINITION mRNA sequence. BI871711 B1871711 731 bp m 603395825F1 NIH_MGC_90 Homo sapiens mRNA nRNA linear EST 11-OCT-2001 cDNA clone IMAGE:5405478 5',

ACCESSION VERSION KEYWORDS EST BI871711.1 GI:16045386

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SOURCE ORGANISM

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em_gss_other:*
em_gss_pro:*

REFERENCE AUTHORS TITLE Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 731) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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//tab_hos!="DH10B (phage-resistant)
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//site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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NJH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection of Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Location/Qualifiers
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Plate: LLAM12034 row: a column: 12
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/note="Organ: liver; Vector: pcwv-SpoRT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies
Note: this is a NIH_MGC Library."

a 240 c 227 g 136 t
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                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 777) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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mRNA sequence.
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CCGGGCTGGGCTCTACTGCTGTCAGGTGCACTTTGATGAGGGGAAGGCTGTCTA
                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Pissue procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LLAM11517 row: c column: 18
High quality sequence stop: 772.
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National Institutes of Health, Mammalian Gene
Unpublished (1999)
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Site_1: NotI; Site_2: EcoRV (destroyed); RNA source
anonymous pool of 24 week female lung, 16 week female
spleen, and 20-22 week male spleens. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 026. Note:
this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5206217"
/clone_lib="NIH_MGC_122"
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                                Similarity:
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CDNA Library Preparation: Michael J. Brownstein (NHGRI), Sh

Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAMAI1722 row: k column: 13

High quality sequence stop: 776.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                          /note-"organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag p); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library." a 278 c 223 g 172 t
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5285892"
/clone_lib="NIH_MGC_96"
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/lab_host="DH10B"
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                                                                found through .... http://image.llnl.gov
http://image.llnl.gov
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plate: plate: row: p column: 20
High quality sequence start: 17
High quality sequence stop: 724.
Location/Qualifiers
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                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLA
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                            Mammalia; Eutheria; Rodentia; St
1 (bases 1 to 918)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, I
                                                                                                                                                                                                                                                                                         house mouse.
Mus musculus
Eukaryota; Metazoa;
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                                                                                                                                          through the I.M.A.G.E. Consortium/LLNL
/organism="Mus musculus"
/strain="FVB/N"
/db_xxef="caxon:10090"
/clone="IMAGE:4206595"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
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Mammalian
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Mammalia; E
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Site_2: Sall; Cloned unidirectionally. Primer:
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library.'
a 292 c 268 g 204 t 1 others
; Metazoa;
Eutheria;
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Catarrhini; Hominidae
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ArgLeuCysGlnValSerGlyLeuLeuAlaLeuArgProGlySerSerLeuArgIleArg
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://imagge.llnl.gov
http://imagge.llnl.gov
plate: LLCM2466 row: n column: 17
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Tissue Procurement: Dr. Mark Watson
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Contact: Robert Strausberg, Ph.D.
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/lab_host="DH10B (phage-resistant)"
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM13607 row: j column: 17
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Tissue Procurement: Dr. James R. Lupski
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/dev_stage="adult, 70 yr"
/lab_host="DH10B"
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AW763237
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                                                                                     Unpublished (1997)
Other_ESTs: ur70d09.xl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.E.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNNL at:
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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US-09-245-198A-4 (1-284) x AW763237
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AGENCOURT_8303564 NIH_MGC_102
5', mRNA sequence.
BQ671259
BQ671259.1 GI:21782093
                                            BQ671259
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/db_xref="taxon:10090"
/clone="IMAGE:315533"
/clone_1ib="NCI_CGAP_Mam3"
/tissue_type="tumor, gross tis
/dev_stage="10 months"
/lab_host="DH10B"
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22, 37-43 (1999) 100 t 1 others
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                                                                                                                                                                                                                                                                                                                                   AlaHisTyrGluValHisProArgProGlyGlnAspGlyAlaGlnAlaGlyValAspGly 163
              LeuArgCysLeuGluGluPheSerAlaThrAlaAlaSerSerLeuGlyProGlnLeuArg
                                                                          TTTGATGAGGGGAAGGCTGTCTACCTGAAGCTGGACTTGCTGGTGGATGGTGTGCTGGCC
                                                                                                                                                        CAGATCGGGGAGTTTATAGTCACCCGGGCTGGGCTCTACTACCTGTACTGTCAGGTGCAC
                                                                                                                                                                                                                                    ACAGTGAGTGGCTGGGAGGAAGCCAGAATCAACAGCTCCAGCCCTCTGCGCTACAACCGC
                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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plate: LLCM2456 row: 1 column: 13
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Location/Qualifiers
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Tissue Procurement: ATCC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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/clone="IMAGE:6274716"
/clone="IMAGE:6274716"
/clone="IMAGE:6274716"
/clone=libb="NIH_MGC_102"
/tissue_type="epidermoid carcinoma, cell line"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="D110B (phage-resistant)"
/lab_host="D10B (phage-resistant)"
/note="Organ: salivary gland; vector: pOTB7; Site_1: xhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-CDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12786 row: p column: 02
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5', mRNA sequence.
BM921213
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Tissue Procurement: Life Technologies,
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/db_xref="taxon:9606"
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/clone_lib="NIH_MGC_115"
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                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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BQ674188
                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LINL http://image.lini.gov
Plate: LLCM2459 row: d column: 01
High quality sequence stop: 335.
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AGENCOURT_8354100 NIH_MGC_102 Homo
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                165
         /tissue_type="epidermoid carcinoma, cell line"
/lab_host="DBHOB (phage resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5: adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
a 286 c 315 g 184 t 1 others
                                                                                                                                                                                  /clone="IMAGE:6275664"
/clone_lib="NIH_MGC_102"
                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rLeuProTrpAlaHisLeuLysAlaAla-ProPheLeuThrTyrPheGlyLeuPhe
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                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11470 row: C column: 17
                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies,
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603047966F1 NIH_MGC_116 Homo
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                                             quality sequence stop:
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1. .785
/organism="Homo sapiens"
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                              GlyAlaValArgGlnAlaGlnProProAlaProMetAla-AlaArgArgSerGlnArgAr
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rAlaAla-SerSerLeu-GlyProGlnLeuArgLeuCysGlnValSer-GlyLeuLeu-A 252
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/clone="IMAGE:5188168"
/clone_lib="NIH_MGC_116"
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                                 SeralaargArgLeuProLeuProArgSerLeuGlySerArgAspGlyGlyAlaValArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution in MGC clone distribution in MGC clone distribution in the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCM1625 row: p column: 08 High quality sequence stop: 587.
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1 (bases 1 to 587)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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602638232F1 NIH_MGC_48 Homo :
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                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="IMAGE:4766071"
//clone=lib="NIH_MGC_48"
//tissue_type="primary B-cells from tonsils (cell line)"
//tissue_type="primary B-cells from tonsils (cell line)"
//lab_bost="PH10B (phage-resistant)"
//note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Rawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Alzawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
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                                /tissue_type="retina"
/clone_lib="RIKEN full-length enriched
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Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hori,F., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kuriharz,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagama,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yashida,K., Yoshida,K., Yoshino,M., Muramatsu,M. and
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Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B. Retina RNA was provided by Stefano Gustincich (Department of Neurobiology, Harvard Medical School, 'About and Boston, MA 02115, USA) whose assistance is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through two rounds of normalization to Rot = 20.0 and subtraction to Rot = 458.8. Second strand cDNA was prepared with the primer adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapter of sequence [5' adapt
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Retina RNA was provided by Stefano Gustincich (Department
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/db_xref="FANTOM_DB:A930030D13"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier B.C., Siden Kilamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Rubin G.M., Venter J.C.;
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Smith H.O.,
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RESULT
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01-OCT-2000 (TrEMBLrel. 15, Cre
01-OCT-2000 (TrEMBLrel. 21, Las
01-JUN-2002 (TrEMBLrel. 21, Las
Hypothetical protein SCO2220.
SCO2220 OR SC10B7,15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 417:141(2002).
Nature 417:141(2002).
RMBL; AL356832; CAB92661.1;
InterPro; IPR002886; Peptidase_M37.
Pfam; PF01551; Peptidase_M37; 1.
SEQUENCE 565 AA; 58070 MW; 7D04:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quali M.A., Kieser H., Harris D.E., Quali M.A., Kieser H., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J., Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
STRAIN=A3(2) / M145;
BentLey S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L
Thomson N.R., James K.D., Harris D.E., Quall M.A., Kleser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Colli
                                                                                                                        Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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"A set of ordered cosmids and a detailed genetic athe 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21:77-96(1996).
                                                                                         Actinomycetales;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                     Q9KZ17
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                                                              SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the model actinomycete Streptomyces
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                                                                                                                                                                                                                                                                                                                                   STGPHLH---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVHPRPGQDG-------AQAGVDGTVSGWEEARINSSSPLRYNRQIGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -VPLALGL---GLALACLGLLLAVVSLGSRASLSAQEPAQEE-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GQAGINWMSSHTGIDFPVLQGTTVMAATDGTVR--
                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                   ---FEVRPAGGSSIDPLPW
                                                                                                           Streptomycineae;
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21.2%;
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7D0418D480C6A284 CRC64;
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                                                                                                                                                                                                     sequence update)
                                                                                                           Streptomycetaceae;
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                                                                                                            Streptomyces.
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Matches 68
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01-MAY-2000
01-MAR-2002
                                                                                              "Genome sequence of the radioresistant radiodurans R1."; Science 286:1571-1577(1999).
                                                                                                                                           MEDLINE=20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D. Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L. Dodson R.J., Haft D.H., Jiang L., Pamphile W., Crosby M., Shen M., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Vamathevan K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R. Makarova K.S., Aravind L., Daly M.J., Smith H.O., Venter J.C., Frager C. M.
                                                                                                                                                                                                                                                                       Bacteria; Thermus/Deinococcus Deinococcaseae; Deinococcus. MCBI_TaxID=1299;
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Nature 417:141-147(2002).
EMBL; AL355732; CAB90868.1;
                                                 Hypothetical protein; SEQUENCE 375 AA; 3
                                                                                                                                                                                                                                                                                                                                                                                                   Q9RRH5
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                                                                                                                                                                                                                                                                                                                            Hypothetical DR2516.
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Rabbinowitsch E., Rajandream A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Ta
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhil
                                                                          TIGR; DR2516;
                                                                                     EMBL; AE002081; AAF12062.1;
                                                                                                                                      Fraser C.M.;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               Deinococcus radiodurans.
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 69; Conser
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643 AA; 6
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  Conservative
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            24.0%;
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  27;
Score 100.5; D
Pred. No. 1.7;
27; Mismatches
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Pred. No. 3;
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                                              proteome.
197B397658ED30B3 CRC64;
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Parkhill J.,
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O'Neil s
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 107;
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                                                                                                                                                                                             D.L.,
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Best Local
 Matches
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Q9JJ15;
Q1-OCT-2000 (TrEMBLrel. 1:
01-OCT-2000 (TrEMBLrel. 1:
01-MAR-2002 (TrEMBLrel. 2:
                                                                   ProDom; PD000001; Euk_pkinase; 1.
ProDom; PD000066; SH3; 1.
SMART; SM00326; SH3; 1.
SMART; SM00326; TYJTKC; 1.
SMART; SM00219; TYJTKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; SH3 domain; Serine,
                                                                                                                                                                                                                                                                          -: SIMILARITY: BELONGS TO THE SER/THE-
-: SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; AF155142; AAF73281.1; -.
HSSP; P29355; 1SEM.
                                                                                                                                                                                                                                                                                                                                       genes and 19.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                SEQUENCE
                                                           Transferase
                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                      Pfam; PF00069; pkinase; Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                             InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkir
InterPro; IPR001252; SH3.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                           Cytogenet. Cell Genet.
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20354997;
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLK3
                                                                                                                                                                                          PRINTS; PR00452;
                                                                                                                                                                                                                                                                                                                                                               "Genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---PSATGEQTHLSLVAPGPGPRDPDWLPWQLALTALSGGSASRLFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVADADAQEVYELVAGLFADWQPGEDRPMPAHFQPGLRLHL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RARRAIAAHYEVHPR-PGQDGAQAG--VDGTVSGWEEARINSSSPLRYNRQIGE-----F 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATAASSLGPQLRLCQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TDRLAVQARAATFPRLPGDPGAGFGHPISGTLAGLE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVVTRPTLPAGELPTLLDLAR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLGSRASLSACE-PAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRGHRCQPTPGRAATARRLRRPGRAPGRRGQPGSHPAARQRLRADLGAALA-----LVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IVTRAGLYYLY
                                                                                                                                                                              PR00452; SH3DOMAIN.
PR00109; TYRKINASE.
            Similarity
                                                                                                                                                                                                                                                                                                                                            19/OLA;
20354997; PubMed=10894943;
A., Ferraz C., Demaille J., Scherer G.,
sequencing reveals the structure of the
sequencing reveals to the Sipal gene
                                               850
 Conservative
                                               AA;
                                               93199 MW;
           6.9%;
                                                                                                                                                                                                                                                    Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                           89:85-88(2000)
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15,
20,
 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last
            Score 100;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; I
Sciurognathi; Muridae;
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                                              8F026CB3532DC10E CRC64;
                                                                                                                                                                                                                                                                                                                SER/THR
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -COVHFDEGKAVYLKLDLLVDGVLALRCLEEFS
                                                                     Serine/threonine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence update)
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73;
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Kcnk6 and
on mouse c
                      Length
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Murinae;
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                        850;
                                                                       kinase;
                                                                                                                                                                                                                                                                                                                                                  chromosome
 38;
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Gaps
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19

LGSRDGGAVRQAQPPAPMAARRSQRRRG----RRGEPGTALLVPLALGLGLALACLGLLLLA

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RESULT 7
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Best Local
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STRAIN-ANTCC 19089 / CB15;

STRAIN-ANTCC 19089 / CB15;

MEDILINE-21173698; pubMed=11259647;

MEDILINE-21173698; pubMed=11259647;

Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

Elsen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

Potocka I., Nelson W.C., Newton A.S., Gwinn M.L., Haft D.H.,

Rolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

Utterback T., Tran K., Wolf A., Venathevan J., Ermolaeva M., White O.

Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

"Complete genome sequence of Caulobacter crescentus.";

Proc. Nacl. Acad. Sci. U.S.A. 98:4136-4141(2001).
  Q8WUI4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003997; RtxD. PRINTS; PR01490; RTXTOXIND.
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01-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caulobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caulobacter crescentus.
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                                                                                              VVATVAGRVAALPVEAGQTVGVGAAVAVLTPGDSALVAEL-YAPSRAAGFV
                                                                                                                                      RLCQVSGLLA---
                                                                                                                                                                              GEV-
                                                                                                                                                                                                              GEFIVTRAGLYYLYCQVHFDEGKAVYLKLDL---LVDGVLALRCLEEFSATAASSLGPQL
                                                                                                                                                                                                                                                    TERLTLARAEVARAETIAAQGFLSPRE----LQARRSAELAVQQEASTLSSQALSYERQI
                                                                                                                                                                                                                                                                                          KGRKTRAR-----RAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQI 185
                                                                                                                                                                                                                                                                                                                                                                     VVSLGSRASLSAQEPA--QEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRS--AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGSRDGGAVRQAQPPAPMAARRSQRRRGRR----GEPGTALLVPLALGLGLALACLGLLLA 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGSPSTPPALNGNPPRPSPEPEEPRRAGPTERGNSSGTPKLIQRALLRGTA-----LLA
                                                                                                                                                                                                                                                                                                                                 --SLGAQSSAAGSRAAATQAALAAESRQ------LTQRRAALNRELAEAKRSLALQ 129
                                                                                                                                                                                                                                                                                                                                                                                                             LAARQGGIVANVHV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CC0683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AE005743; AAK22668.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria; alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 378 AA; 39659 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secretion protein.
      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                        -----DARLAAIPIDLQAARAEAASTLAGLEQ-QATQVEAQGRYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.9%;
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17, Last sequence up
20, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 99.5;
Pred. No. 2.
    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                             REGDRVVVGQPIATLTLSSALEGGDSFAVLSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subdivision; Caulobacter group;
                                                                                                                                      -LRPGSSLRIRTLPWAHLKAAPFL
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  614
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01-OCT-2000
01-OCT-2000
01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-B-CELL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-COLON;
                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NPQT - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELQSVHSERH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46;
                      855
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QBWUI4: Q9BR73;
01-MAR-2002 (TrEMBLrel. 2
01-MAR-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
Histone deacetylase 7A.
           Li S., Fischle W., Verdin E., Walsh M.J.;
A novel class II HDAC is associated with the transcript homeodomain repressor CCAAT displacement protein.";
submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF239243; AAF63491.1;
InterPro; IPR000286; His_deacetylse.
Piam; pr00850; Hist_deacetylse.
PRINTS; PR01270; HDASSPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Histone deacety.
Homo sapiens (Human).
Homo sapiens (Human).
'--rvota; Metazoa; Chordata;
'--rvota; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (APR-2001) to the EMBL/Ger EMBL; BC020505; AAH20505.1; EMBL; BC006453; AAH06453.1; InterPro; IPR000286; His_deacetylse.
                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00850; Hist_deacetyl; PRINTS; PR01270; HDASUPER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (JAN-2002)
                                                                                                                                                             TISSUE-CERVICAL CARCINOMA;
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            Histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 339-614 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRGSTGDTVLLPLAQGGHRPLS-----RAQSSPAAPASLSAPEPASQARVLSSSETPART 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPFTTGLIYDSVMLKHQCSCGDNSRHPEHAGRIQSIWSRLQERGLRSQCECLRGRKASLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -RGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSEL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RQIPSAEDLETDGGGPGQVVDDGLEHRELGHGQPEARGPAPLQQHPQVLLWEQQRLAGRL 122
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AA;
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                                                                                                                                                                                                                                     Chordata;
Primates;
92363
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Last annotation updat
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
3157426AE1913DB6 CRC64;
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Best Local
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Best Local
Q9S2W5
Q9S2W5;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Koehrer K., Beyer A., Mewes H.W., Gassenhuber J., Wiemann Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AL117455; CAB55935.1; -
Interpro; IPR000286; H1s_deacetylse. Pfam; PF00850; H1st_deacetyl; 1. PF1NTS; PR01270; HDASUPER.
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DKFZP586J091/,
Homo sapiens (Human).
Homo sapiens (Homan).
Horia; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last sequence 01-DEC-2001 (TrEMBLrel. 19, Last annotation of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the con
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01-MAY-2000 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                       -RGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSEL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
46; Conserv
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     (TrEMBLrel.
                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                          EESQDP - -
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     Created)
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Pred. No. 6.2;
21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -QAQPPAPMAAR-----RSQRRRGR- 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
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                                                   B
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                                                                                                                                                                                                                                                                                                                          APFLNRLVRPRRSAPKGRKTRAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 878;
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Q96JP2
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Best Local
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                    Q96JP2 PRELIMINARY;
Q96JP2;
Q96JP2;
O1-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-JUN-2002 (TrEMBLrel. 21, L
KIAA1783 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the mod coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL109563; CAB52000.1; -.
InterPro; IPR002965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Redenbach M., Kieser H.M., Denapaite D., Eichner / Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic at the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapaite D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
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     KIAA1783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hopwood D.A.;
                                                                                                                                                                                                                                                                            104 I-DAYSAPRALQRRAR-----ELGMVPGGDPAFLDPDGTVKGVPSPAPAAATPL
                                                                                                                                                                                                                                                                                                                          124
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nes 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                        GSRDGGAVRQAQPPAPMAARRSQRRRGR------RGEPGTA---LLVPLALGL 63
                                                                                                                                                                                                                                                                                                                                                                           GL----IGLLVL--
                                                                                                                                                                                                                                                                                                                                                                                                                          GLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPRDPGKI-QTTPPRGGRVSRKPELKGRAARLARLLPTGGSRGQAARAPFVLLVVVLLGG 64
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(AUG-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
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Last annotation updat
                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90131DF9AAB059D7
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Streptomycetaceae; Streptomyces
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Taylor K.,

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151

103

16; 64;

Length CRC64;

206;

Indels

46;

Gaps

7;

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Q8S5
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Q8S5I5
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Best Local :
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InterPro; IPR001609; myosin_head.
InterPro; IPR001657; MyTH4.
InterPro; IPR001452; SH3.
InterPro; IPR001452; SH3.
Pfam; PF00612; IQ; 1.
Pfam; PF000613; myosin_head; 1.
Pfam; PF000784; MyTH4; 1.
Pfam; PF00018; SH3; 1.
SMART; SM00015; IQ; 1.
                                                                                                                                                     01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
01-JUN-2002 (TrEMBLrel. 2
Hypothetical 41.5 kDa pro
05JNBA0061H20.4.
Oryza sativa (Rice).
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                                                                                                                                                                                                                                                       Q8S515
           SEQUENCE FROM N.A.
STRAIN-NIPPONBARE;
MCCombie W.R., de la Bastide M., Spiegel L., Prest
Kuit K., Nascimento L., Zutavern T., Balija V., B
Santos L., Miller B., Katzenberger F., Muller S.,
                                                                                                                                                                                                                                                                                                                             1158
                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                    1105
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                                                                                                                                                                                                                                           Q8S5I5;
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                                                                                                 NCBI_TaxID=4530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 RRLPLP----RSLGSRDGGAVRQAQPPA---PMAARRSQRRRG---RRGEPGTALLVPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            large Proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens (Human)
                                                                                                                                                                                                                                                                                                                           KLGINGAHSSPPMLSPSPGKGPPPAVAPRPKAPLQLGPSSSIKEKQGPLLDLFG
                                                                                                                                                                                                                                                                                                                                                      EFSATAASSLGPQLRLCQVSG----LLALRPGSSLRIRTLPWAHLKAAPFLTYFG
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                                                                                                                                                                                                                                                                                                                                                                                                          NSSSPLR--YNRQIGEFI---VTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLE 228
                                                                                                                                                                                                                                                                                                                                                                                                                                       PPPPIVKKPLKQGGAKAPKEAEAEPAKETAA--KGH---GQGPAQG--RGTV-----VRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPAPFLNR-LVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALGLGLALACLGLLLAVVSLGSRASL-----SAQEPAQEELVAEEDQDPSELNPQTEESQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RKPPTPPEKPORDLGS-EGGCLRETSEEAEDRPYOPKSFQQKRNYFQRMGQP------
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                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---QITVRTMKPPAKVHIPQGEAQEEEEEE-EEEEEQEEQEVETRAVPSP 1056
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il. 21, Last sequence update)
il. 21, Last annotation updat
protein.
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uences of unidentified human genes
new cDNA clones from brain which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                        408
                                                                                                                                                                                                                                                        AA
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                       Preston
V., Bell
                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1560;
AR., F
Jll M., F
, King L
          Ferry, Baker J., vang C.,
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which code
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                                                                                                                                                                                                                                                                                                                             1211
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RESULT 13
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                              O9NYAO;
O1-OCT-2000 (TrEMBLrel. 15,
O1-OCT-2000 (TrEMBLrel. 15,
O1-JUN-2002 (TrEMBLrel. 21,
B2 gene partial cDNA, clone
                                                                                                                                                PROSITE; PS00190; CYTOCHROME_C; UNKNO PROSITE; PS50081; DAG_PE_BIND_DOM_2; PROSITE; PS50003; PH_DOMAIN; 1.
SEQUENCE 926 AA; 103198 MW; 66826
                                                                                                                                                                                                                                                                                                                         Hanski C., Gratchev A., Hanski M.L., Hummel M., "Molecular cloning and two PH domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (APR-2002) to the EMEL; AC113337; AAM08840.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dike S., O'Shaughnessy A., Palmer L., "Genomic sequence for Oryza sativa, N OSJNBA0061H20, from chromosome 10, co
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                        GLALACLGLLLAVVSLGSRASL---SAQEPAQEELVAEED-QDPSELNPQTEESQDP---
                                                                        LDFEISARRLPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLALGL
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                                               LHCEAPAEPLPAQAASGTQDGVHVQEPRPQAPSPLDLQQPVESTSGQQPSSTVSETAREV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 26.5 60; Conservative
                                                                                                            Similarity
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-NGLQKAQAHDGAGLKLVVSSPTSPKNKSWISEDDFYRPSREQPLESASDHPIAS
                                                                                                  Conservative
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                                                                                                             24.2%;
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                                                                                                                                                   66B2618C12C3B27B CRC64;
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RESULT 14

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DNA Res. 4:141-150(1997).
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SMART; SM00109; C1; 1.
SMART; SM00233; PH; 2.
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
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InterPro; IPR000532; Glucagon.
InterPro; IPR001494; PH.
InterPro; IPR004012; Run.
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97349984; PubMed-9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=BRAIN;
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VDGVLALRCLEEFSATAASSLGP-----QLRLCQVSGLLALRPGS 257
                                                                                                                                                                                                                                                                            GLALACLGLLLAVVSLGSRASL---SAQEPAQEELVAEED-QDPSELNPQTEESQDP--- 116
                                                                                                                                                                                                                                                                                                                                                                                 LDFEISARRLPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTALLVPLALGL
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                                                                                               WEEARI-----NSSSPLRYNRQIGEFIVTRAGLY----YLYCQVHFDEGKAVYLKLDLL
                                                                                                                                                                                                                                                GQG----NGLQKAQAHDGAGLKLVVSSPTSPKNKSWISEDDFYRPSREQPLESASDHPIAS 468
                                                 HKSFRVVHRRQMGLSNPFRGLMKLG--TVERRGAMGIWKELFCELSPLEFR-LYLSNE--
                                                                                                                                                   YRGTPGSRPGLHRHFSQEPRKNCSLGALDQA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 97; DB 4
Pred. No. 12;
35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic
clone:B1114B07.";
                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; AP003334; BAB90006.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                   -VAG-----RGKSPTVPTRDWS
                                                                            QVSGLLALRPGSSLRIRTLPWA
                                                                                                                             GEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLLVDGVLALRCLEEFSATAASSLGPQLRLC
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                                                                                                                                                                             PRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQI 185
                                                                                                                                                                                                        RGAALAPGSLGRRRGGGQRLAGVGDAEREADGDEGRDPRGVEDRGRRDGEPAEEVALVV-
                                                                                                                                                                                                                              -GLLLAVVSLGSRAS----LSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVR 125
                                                                                                                                                                                                                                                          {\tt LADTAVGLGSDVARRRGHLGCRRGSGGGGGGGGGGGGGGGASHAATAALIPWRGTAPCRG}
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67; Conserv
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              2003,
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Pred. No. 7.7;
33; Mismatches
                                                   388
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7.7;
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Minimum DB Maximum DB Result No. Run Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Total number of hits satisfying chosen parameters: Title: Perfect score: OM protein - protein search, using sw model Database Searched: Scoring table: Sequence: on: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 100.5 99.5 99.9 93.5 93.5 93.5 91.5 91.5 91.5 91.5 88.5 Score 106. seg length: 0 seg length: 2000000000 PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Query Match Length DB BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-245-198A-4 1444 March 31, 2003, 07:44:21; Search time 28.4558 Seconds 283224 seqs, 96134422 residues **あめののののののののののののののののののののの**の MSLLDFEISARRLPLPRSLG.....PWAHLKAAPFLTYFGLFQVH GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. 7899024 138427
S27224
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959.459 Million cell updates/sec 283224 hypothetical prote hypothetical prote 2,4-diencyl-CoA re hypothetical prote cadherin-15 precur conserved hypothet probable inhibitor hypothetical prote hypothetical prote fas ligand - numan probable two-compo conserved hypothet hypothetical prote fas probable two-compo conserved hypothet hypothetical prote tumor necrosis fac lymphotoxin - bovi hypothetical prote hypothetical prote ORF5 protein - Orf probable two-compo hypothetical prote probable membrane mitosis-specific c probable cation-tr 4-1BB ligand hum
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RESULT 2 S27/24 N-methyl-D- C:Species: C:Date: 25- C:Accession R:Ikeda, K. PEBS Lett. A:Title: C1 A:Reference A:Accession	150 103 207 147 147 250	ery st tch	SULT 1 18427 1BB liga 19Becies: Date: 29 Date: 29 Date: 29 Accessio Alderson II. J. Im III. J. Im Referenc Accessio Status: Wolatus: Residues Cross-re	30 30 30 30 30 30 30 30 30 30 30 30 30 3
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lon-4 chain - mouse se) sion 01-Sep-1995 #text ; Araki, K.; Sakimura, the epsilon-4 subunit 1050214; PMID:1385220	PRPGODGAQAGVDGTVSGWEEARINSSPLRNINGIGEFIVTRAGLYYLYCOVH	re 106.5; DB 2; d. NO. 0.32; Mismatches 93; LALGLGLALACLGLLLA LLLLLLLAAACAVFLAC APPLNRLVRPRRSAPKG : AGLLDL	T.W.; Davis-Smith, acterization of hum 434; PMID:8088337	H83357 F83633 B70629 B75346 E98121 S14113 D95256 A60535 B69953 G98331 E83325 E83325 E83325 P75518 B48349 C98227 AE3059
change 17-Mar-1999 , K.; Watanabe, M.; Inoue, Y. of the NMDA receptor channel	SG 249	th 254; ls 81; Gaps GSRASL-SAQE 89 : GARASPGSAAS 67 GRRAIAAHYEVH 14 :: :: AQLVAQNVLL- 10	<pre>change 21-Jul-2000 T.; Armitage, R.J.; Falk, B. an 4-1BB and its ligand. 34.1; PID:g571323</pre>	probable non-ribos hypothetical prote hypothetical prote probable competenc hypothetical prote 1-phosphatidylinos ATP-dependent Clp ClpB-like protein hypothetical prote probable oligopept probable chemotaxi hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote

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Appointerical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
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C:Species: Deinococcus radiodurans
C:Species: Deinococcus radiodurans
C:Species: O3-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: A75264
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Vennter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75264
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-375 < WHI>
A;Cross-references: GB:AE002081; GB:AE000513; NID:g6460337; PIDN:AAF12062.1; PID:g646034
A;Experimental source: strain R1
C:Gene: DR2516
A;Map position: 1
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A;Molecule type: mRNA
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                                                            VVADADAQEVYELVAGLFADWQPGEDRPMPAHFQPGLRLHL--
                                                                                                    IVTRAGLYYLY---
                                                                                                                                         TDRLAVQARAATFPRLPGDPGAGFGHPISGTLAGLE--RLSAASLRAHWARFGQRGSVLG 147
                                                                                                                                                                               RARRAIAAHYEVHPR-PGQDGAQAG--VDGTVSGWEEARINSSSPLRYNRQIGE-----F 188
                                                                                                                                                                                                                       DVVTRPTLPAGELPTLLDLAR------QDLESLDDSP--------
                                                                                                                                                                                                                                                              SLGSRASLSAQE-PAQEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRSAPKGRKT 136
                                                                                                                                                                                                                                                                                                    GAVROAOPPAPMAA-----RRSORRRGERGEPGT--ALLVPLALGLGLALACLGLLLAVV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PKGRKTRARRATAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQIG
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                                                                                                                                                                                                                                                                                                                                                                                     69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                        Score 100.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                  -COVHFDEGKAVYLKLDLLVDGVLALRCLEEFS
-GLLALRPGSSLRIRT
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                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                    231
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R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelber, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; In, J.; Ermolaeva, M.; White, O.; Salberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HlyD family secretion protein [imported] - Caulobacter crescentus C;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001 C;Accession: H87333
                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein DKFZp586J0917.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T17245
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                                                                                                                                                                                                                                                                                                                                                 R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; submitted to the Protein Sequence Database, September 19
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C;Genetics:
  В
                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-878 < KOE>
                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: T17245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-378 <STO>
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                                                                                                                                                                  A; Note:
                                                                                                                                                                                                      A; Experimental source: adult uterus; clone DKFZp586J0917
                                                                                                                                                                                                                           A; Cross-references: EMBL: AL117455
                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                      Query Match
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73;
  327
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                                          11 RRLPLPRSLGSRDGGAVR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 --SLGAQSSAAGSRAAATQAALAAESRQ-----LTQRRAALNRELAEAKRSLALQ 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76
                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 LGSRDGGAVRQAQPPAPMAARRSQRRRGRR----GEPGTALLVPLALGLGLALACLGLLLA 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC0683
                                                                                                                                                              DKFZp586J0917.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGRKTRAR-----RAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPLRYNRQI 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVSLGSRASLSAQEPA--QEELVAEEDQDPSELNPQTEESQDPAPFLNRLVRPRRS--AP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAARQGGIVANVHV-----REGDRVVVGQPIATLTLSSALEGGDSFAVLSR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GEFIVTRAGLYYLYCQVHFDEGKAVYLKLDL---LVDGVLALRCLEEFSATAASSLGPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TERLTLARAEVARAETIAAQGFLSPRE----LQARRSAELAVQQEASTLSSQALSYERQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---PSATGEQTHLSLVAPGPGPRDPDWLPWQLALTALSGGSASRLFT
RQIPSAEDLETDGGGPGQVVDDGLEHRELGHGQPEARGPAPLQQHPQVLLWEQQRLAGRL 386
                                                                                l Similarity
46; Conser
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                                                                                  Conservative
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                                                                                                   6.98;
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                                                                                  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                              Score 99; DB
Pred. No. 5.1;
21; Mismatches
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LRPGSSLRIRTLPWAHLKAAPFL 275
                                        ----QAQPPAPMAAR-----RSQRRRGR- 47
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                                                                                  67;
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                                                                                  56;
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                                                                                  Gaps
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aft, D.H., Ko
C.: Fraser, C
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R; Fobert, P.R.; Coen, E.S.; Murphy, G.J.P.; Doonan, J.H.
EMBO J. 13, 616-624, 1994
A; Title: Patterns of cell division revealed by transcriptional
A; Reference number: S41710; MUID:94148008; PMID:8313906
A; Accession: S41710
A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Residues: 1-441 <FOBS-
A; Cross-references: EMBL:X76123; NID:9425262; PIDN:CAA53770 1
                                                                            A;Gene: cyc2
C;Superfamily
C;Keywords: c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable membrane protein - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999 C;Accession: T34961
R;Saunders, D.C.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Raja submitted to the EMBL Data Library, August 1999
A;Reference number: Z21563
A;Accession: T34961
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                         mitosis-specific cyclin 2 - garden snapdragon c;Species: Antirrhinum majus (garden snapdragon) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 C;Accession: S41710 R;Fobert, P.R.; Coen, E.S.; Murphy, G.J.P.; Doonan,
                                                                                                                                                                                                                                                                                                                                  RESULT
S41710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-206 <SAU>
                                                                           Superfamily: cyclin
Keywords: cell cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                 104
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                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                                                                                                                                                                                                                                                                                I-DAYSAPRALQRRAR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GSRDGGAVRQAQPPAPMAARRSQRRRGR------RGEPGTA----LLVPLALGL 63
                                                                                                                                                                                                                                                                                                                                                                                                                            VRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGTVSGWEEARINSSSPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPSELNPQTEESQDPAPFLNRL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELQSVHSERH 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           GL----IGLLVL----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
48; Conserv
                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                            control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%;
                                6.7%;
24.0%;
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                                                                            cell division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18;
               44;
                               Score 97;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                -ELGMVPGGDPAFLDPDGTVKGVPSPAPAAATPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----NSALSEGSFQLDDLKQRTKELTDEEQALQRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 98; DB Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                 Mismatches
                                3.4;
                                               DB 2;
                                                                            control; mitosis
                                                                                                                                     PIDN:CAA53729.1; PID:g425263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
                  104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64; Indels
                                             Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                  Indels
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                                                                                                                                                                                                                             regulation
                  74;
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                                                                                                                                                                                                                                                                                                                                                                                                151
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                  Gaps
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                  15;
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hypothetical protein C54D2.5 - Caenorhabditis elegans C;Speciaes: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #t.C;Accession: T15838 R;Minx, P.
                                                                           RESULT
T15838
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T36946
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                                                                                                                                      В
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A; Residues: 1-776 <SEE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
63; Conserv
                               #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
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C; Superfamily: ATPase nuc
F;442-585/Domain: ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Seeger, K.J.; Harris, D.; Thomson, submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable cation-transporting ATPase - Streptomyces
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
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LVVATPCPLLLAAPVAVVSGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIN-IVDRYLASKTTSRRELQLLGMSSMLIASKYEEIWAPEVNDLVCISDGS
                                                                                    TYAGIVRL-----AQQAGAESAPVVRLADRYAAWFLPLALATAALAWLVSGSAVRAVAV
                                                                                                                              LVDGVLALRCLEEFSATAASSLGPQLRLCQ--
                                                                                                                                                                         RVESTEAVLDESVLTGEPLQVTRQRGEGARSGAVNAGGAFDL
                                                                                                                                                                                                                                                              RSARRTGDG-----VVR----VPLSEITAGDALVVGPGEVVP------VDG
                                                                                                                                                                                                                                                                                                        SELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDG 163
                                                                                                                                                                                                                                                                                                                                                   RRGEPGTALLVPLALGLGLALA--CLGLLLA-VVSLGSRASLSAQEPAQEELVAEEDQDP 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLDLLVDGVLALRC-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --APVLEKEITGEKSLKKKAPTLTSTLTARSKAASV-VRTKPKEQIVDIDAADVNNDLAV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPAPFLNRLVRPRRS----APKGRKTRARRAIAAHYEVHPRPGQ-----DGAQAGVDGTV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAIKQKS----MAVEKKNRRALGDIGNVVTVRGVEGKALPQVSRPITRGF-----CAQLI 69
                                         -IRTLPWAHLKAAPFLTYFGL
                                                                                                                                                                                                                   TVSGWE---EARINSSSPLRYNRQIGE----FIVTRAGLYYLYCQVHFDEGKAVYLKLDL 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANAEAAAAENNKNSLAVNAKGADGALPIKRAVARVPVQKKTVKSKPQEIIEISPDTEKKK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATPase nucleotide-binding don in: ATPase nucleotide-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           30;
                                         280
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 93.5;
Pred. No. 12
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ber 1999
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                                                                                                                                -----VSGLLALRPGSSLR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 776;
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                                                                                    274
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submitted to the EMBL Data Library, October 1995
A; Description: The sequence of C. elegans cosmid C54D2.
A; Reference number: Z18415
A; Accession: T15838
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1657 <MIN
A; Cross-references: EMBL:U37548; NID:g1017804; PID:g101780
C; Genetics:
A; Gene: CESP:C54D2.5
A; Introns: 40/2; 67/3; 86/3; 121/2; 199/3; 230/2; 308/2; C; Superfamily: sodium channel protein
                                                                                                                                                                                                                                                                                                      A;Cross-references: (
A;Experimental source
C;Genetics:
A;Gene: Rv0497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10

770745

G:Species: Mycobacterium tuberculosis (strain H37RV)

G:Species: Mycobacterium tuberculosis
G:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
G:Accession: D70745
G:Accession: D70745
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Deviin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
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A;Accession: D70745
A;Status: preliminary; nucleic acid sequence not shown; translation not A;Molecule type: DNA
A;Residues: 1-310 <COL>
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Best Local
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                                                                                    48
                                                                                                                                                                    DQDPSELNPQTEESQDPAPFLNRLVRPRR----SAPKGRKTRARRAI---AAHY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGAQAGVDGTVSGWEEARINSSSPL-------RYNRQIGEFIVTRAGLYYLYCOV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTALLVPLALGLGLALACLG-----LLLAVVSLGSRAS-----LSAQEPAQEELVAEED 100
                                     AGPDAHASQSPAANGR------VQVGEAAPQSPAEPVAEQ-VAEEPTRTVYWS 109
                                                                                  RGEPGTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEE-----
                                                                                                                            PETESSGNRQISVAELLARQGVTGAP--ARRRRRRGDSDAITVAELTGEIPIIRDDHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --LFLMGPKNPLRIKCLQTTQKKWFDYTVLF 1124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KHS-ANLDAIID--KRLVLRNSAPFDRSPVSEGRDDSRLNRHASLVLPVANGVPYRRQRV 1051
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GMAQTNPWAALYFVALMTFGNYVLFNLLVAILVEGFQESKEEEKRQLEEDARKQAVEEED 940
                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                     6.48;
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23.2%;
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                                                                                                                                                                                                                                     Score 93;
Pred. No.
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Pred. No. 29;
                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                       Length 310
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                                                                                                                                                                                                               Gaps
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A;Gene: SCOEDB
C;Superfamily:
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R;Fraser, K.M.; Hill, D.F.; Mercer, A.A.; Robinson, A.J.
Virology 176, 379-389, 1990
A;Title: Sequence analysis of the inverted terminal repetition
A;Reference number: A34768; MUID:90266454; PMID:2129563
                                                                                                                                                                                                                                      probable two-component sensor - Streptomyces coelicolor
C; Species: Streptomyces coelicolor
C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #tex
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                                                                                                          A; Molecule type: DNA
A; Residues: 1-566 <SEE>
                                                                                                                                                                                      R;Seeger, K.; Harris, D.; Parkhill, J.; Barrell, submitted to the EMBL Data Library, April 1998
                                                                                                                                                                                                        C; Accession:
R; Seeger, K.;
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A; Status: preliminary
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C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change
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                                                                                            A; Cross-references:
                                                                                                                                                        A; Accession: T35203
                                                                                                                                                                         A; Reference number: Z21571
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A; Residues: 1-351 <FRA>
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45; Conserv
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                        two-component sensor histidine kinase;
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                                                                                            PIDN:CAA18527.1; GSPDB:GN00070;
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Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein Rv1219c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: A70611
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.;
Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Hc
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
hypothetical protein PA3305 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: D83231
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A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv1219c
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26; Mismatches
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4; Mismatches
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A;Reference number: A82950;
A;Accession: H83044
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                                                                     Qy
                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-681 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2,4-dienoyl-CoA reductase FadH2 PA4814 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa
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                                                                                                                                                                                                                       C; Superfamily:
                                                                                                                                                                                                                                        A; Gene: fadH2;
                                                                                                                                                                                                                                                           C; Genetics
                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE004894; GB:AE004091; NID:g9951076; PIDN:AAG08199.1; GSPDB:GNA;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: H83044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: PA3305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-664 <STO>
                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE004753; GB:AE004091; NID:g9949433; PIDN:AAG06693.1;
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Best Local Similarity
Matches 77; Conserv
498
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VLRGAPVGARVAIVGAGGIGFDVA--AFLVAAPSDG---
                                --RGEP-GTALLVPLALGLGLALACLGLLLAVVSLGSRASLSAQEPAQEELVAEEDQDPS 104
                                                                     FRVRLERLGVDLRLGHR----VRQGELDGQFDDVVVATGIQPRRPRIDGIGGPTVLSYVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RQRQPQGLLNALSKIVEVDAQRDHAWFEGERGRRRAGALALLSRDLLSL-----LRT
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                                                                                                           FEISARRLPLPRSLGSRDGGAVRQAQPPAP----MAARRSQRRRGR-----
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                                                                                                                                              l Similarity
79; Conserv
                                                                                                                                                                                                                                        PA4814
                                                                                                                                                                                                                     Methylophilus methylotrophus
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                                                                                                                                                                                                                                                                                                                                                                                      sequence of Pseudomonas aeruginosa 50; MUID:20437337; PMID:10984043
                                                                                                                                                               6.3%; Score 91;
26.3%; Pred. No.
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25.8%;
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Pred. No. 15;
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                                                                                                                                                Mismatches
                                                                                                                                                                 DB 2; Length 681, 17;
                                                                                                                                                                                                                     W3A1 trimethylamine
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K.R.; Kas,
                                                                                                                                                                                                                                                                                                                                                                                                        PA01,
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Larbig,
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Larbig,
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Db	Qy	ф	οy	DЪ	ρ
627	218	584	165	549	105
627 VDNVVICAGQEPLRELQIRQATESLRFHLIGGARVAGELDAKRAIREGAMLAAR 680	218 VDGVLALRCLEEFSATAASSLGPQLRLCQVSGLLALRPGSSLRIR 262 .	584 TSGWVHRAHLRHNAVRMLGGVEYLKIDE-RGLLIRVDGVERWLE 626	165 VSGWEEARINSSSPLRYNRQIGEFIVTRAGLYYLYCQVHFDEGKAVYLKLDLL 217		105 ELNPQTEESQDPAPFLNRLVRPRRSAPKGRKTRARRAIAAHYEVHPRPGQDGAQAGVDGT 164
580	262 .	526	217	583	164

Search completed: March 31, 2003, 07:59:21 Job time: 34.4558 secs

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Schnizer, Richard

Sent:

Friday, March 14, 2003 6:45 AM STIC-Biotech/ChemLib

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Subject:

09/245,198

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Please perform an oligo search on SEQ ID NO:4.

Please also search for nucleic acids that can encode the amino acid sequences of SEQ ID NOS:2 or 4.

Thank you-

Richard Schnizer, Ph.D. Patent Examiner Art Unit 1635 CM1 12E17 703-306-5441 Mail Box CM1 11E12

> Point of Contact: Thomas G. Larson, Ph.D. 703-308-7309 CM1, Rm. 6 B 01

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Phone:
Location:
Date Picked Up: 3/24
Date Completed: <u>リ</u> //
Searcher Prep/Review: 15
Clerical:
Online time: 20

TYPE OF SEARCH:, /
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.: 43
WWW/Internet:
Other (specify):

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